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(54) Title: METASTATIC BREAST AND COLON CANCER REGULATED GENES		
(57) Abstract Gene sequences as shown in SEQ ID NOS:1-85 have been found to be significantly associated with metastatic potential of cancer cells, especially breast and colon cancer cells. Methods are provided for determining the risk of metastasis of a tumor, which involve determining whether a tissue sample from a tumor expresses a polypeptide encoded by a gene as shown in SEQ ID NOS:1-85, or a substantial portion thereof.		

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METASTATIC BREAST AND COLON CANCER REGULATED GENES

TECHNICAL FIELD OF THE INVENTION

This invention relates to methods for predicting the behavior of tumors. More particularly, the invention relates to methods in which a tumor sample is
5 examined for expression of a specified gene sequence thereby to indicate propensity for metastatic spread.

BACKGROUND OF THE INVENTION

Breast cancer is one of the most common malignant diseases in women, with about 1,000,000 new cases per year worldwide. Colon cancer is another of the
10 most common cancers. Despite use of a number of histochemical, genetic, and immunological markers, clinicians still have a difficult time predicting which tumors will metastasize to other organs. Some patients are in need of adjuvant therapy to prevent recurrence and metastasis and others are not. However, distinguishing between these subpopulations of patients is not straightforward, and course of treatment is not
15 easily charted. There is a need in the art for new markers for distinguishing between tumors which will or have metastasized and those which are less likely to metastasize

SUMMARY OF THE INVENTION

It is an object of the present invention to provide markers for distinguishing between tumors which will or have metastasized and those which are less
20 likely to metastasize. These and other objects of the invention are provided by one or more of the embodiments described below.

One embodiment of the invention provides an isolated and purified human protein having an amino acid sequence which is at least 85% identical to an amino acid sequence encoded by a nucleotide sequence selected from the group
25 consisting of SEQ ID NOS:1-63 or the complement thereof.

Another embodiment of the invention provides a fusion protein which comprises a first protein segment and a second protein segment fused to each other by

means of a peptide bond. The first protein segment consists of at least six contiguous amino acids selected from an amino acid sequence encoded by a nucleotide sequence selected from the group consisting of SEQ ID NOS:1-63 or the complement thereof.

Yet another embodiment of the invention provides an isolated and
5 purified polypeptide consisting of at least six contiguous amino acids of a human protein having an amino acid sequence encoded by a nucleotide sequence selected from the group consisting of SEQ ID NOS:1-63 or the complement thereof.

Still another embodiment of the invention provides a preparation of antibodies which specifically bind to a human protein which comprises an amino acid
10 sequence encoded by a nucleotide sequence selected from the group consisting of SEQ ID NOS:1-63 or the complement thereof.

Even another embodiment of the invention provides an isolated and purified subgenomic polynucleotide comprising at least 11 contiguous nucleotides of a nucleotide sequence which is at least 96% identical to a nucleotide sequence selected
15 from the group consisting of SEQ ID NOS:1-63 or the complement thereof.

Another embodiment of the invention provides an isolated and purified gene which comprises a coding sequence comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS:1-63 or the complement thereof.

Yet another embodiment of the invention provides a method for
20 determining metastasis in a tissue sample. An expression product of a gene which comprises a coding sequence selected from the group consisting of SEQ ID NOS:1, 2, 4, 5, 9, 11, 13, 14, 18, 19, 20, 22, 24, 26, 29, 30, 33, 35, 36, 38-41, 45, 48, 52, 55, 57, 58, 60, 63-66, 69-74, 76, 80, 82, and 83 is measured in a tissue sample. A tissue sample which expresses the product is categorized as metastatic.

25 Still another embodiment of the invention provides a method for determining metastasis in a tissue sample. An expression product of a gene which comprises a sequence selected from the group consisting of SEQ ID NOS:3, 7, 8, 10, 12, 15-17, 21, 23, 28, 31, 34, 37, 42-44, 46, 47, 49-51, 53, 59, 61, 62, 67, 68, 75, 77-79, 81, 84, and 85 is measured in a tissue sample. A tissue sample which does not express
30 the product is categorized as metastatic.

Even another embodiment of the invention provides a method for determining metastatic potential in a tissue sample. An expression product of a gene which comprises a sequence selected from the group consisting of SEQ ID NOS:1, 2, 4, 5, 9, 11, 13, 14, 18, 19, 20, 22, 24, 26, 29, 30, 33, 35, 36, 38-41, 45, 48, 52, 55, 57, 58, 60, 63-66, 69-74, 76, 80, 82, and 83 is measured in a tissue sample. A tissue sample which expresses the product is categorized as having metastatic potential.

A further embodiment of the invention provides a method for determining metastatic potential in a tissue sample. An expression product of a gene which comprises a sequence selected from the group consisting of SEQ ID NOS:3, 7, 8, 10, 12, 15-17, 21, 23, 28, 31, 34, 37, 42-44, 46, 47, 49-51, 53, 59, 61, 62, 67, 68, 75, 77-79, 81, 84, and 85 is measured in a tissue sample. A tissue sample which does not express the product is categorized as having metastatic potential.

Another embodiment of the invention provides a method of predicting the propensity for metastatic spread of a breast tumor preferentially to bone or lung. An expression product of a gene which comprises a sequence selected from the group consisting of SEQ ID NO:1, 5, 11, 18, 20, 22, 24, 30, 33, 35, 36, 38, 45, 52, 58, 65, 66, 70, 74, 76, and 80 is measured in a breast tumor sample. A breast tumor sample which expresses the product is categorized as having a propensity to metastasize to bone or lung.

Even another embodiment of the invention provides a method of predicting propensity for metastatic spread of a breast tumor preferentially to lung. An expression product of a gene which comprises a sequence selected from the group consisting of SEQ ID NOS:2, 4, 9, 13, 14, 19, 26, 29, 39-41, 48, 55, 57, 60, 63, 64, 72, 73, 82, and 83 is measured in a breast tumor sample. A breast tumor sample which expresses the product is characterized as having a propensity to metastasize to lung.

Still another embodiment of the invention provides a method of predicting propensity for metastatic spread of a colon tumor. An expression product of a gene which comprises the nucleotide sequence shown in SEQ ID NO:56 is measured in a colon tumor sample. A colon tumor sample which expresses the product is characterized as having a low propensity to metastasize.

Even another embodiment of the invention provides a method for determining metastasis in a tissue sample. An expression product of a gene which comprises a coding sequence selected from the group consisting of SEQ ID NOS:3, 7, 8, 10, 12, 15-17, 21, 23, 25, 28, 31, 34, 37, 42-44, 46, 47, 49, 61, 62, 67, 68, 75, 77-79, 81, 84, and 85 is measured in a tissue sample. A tissue sample which expresses the product is categorized as non-metastatic.

Yet another embodiment of the invention provides a method for determining metastasis in a tissue sample. An expression product of a gene which comprises a coding sequence selected from the group consisting of SEQ ID NOS:3, 7, 8, 10, 12, 15-17, 21, 23, 25, 28, 31, 34, 37, 42-44, 46, 47, 49, 61, 62, 67, 68, 75, 77-79, 81, 84, and 85 is measured in a tissue sample. A tissue sample which does not express the product is categorized as metastatic.

The invention thus provides the art with a number of genes and proteins, which can be used as markers of metastasis. These are useful for more rationally prescribing the course of therapy for breast or colon cancer patients.

DETAILED DESCRIPTION

It is a discovery of the present invention that a number of genes are differentially expressed between metastatic cancer cells, especially cancer cells of the breast and colon, and non-metastatic cancer cells. These genes are metastatic marker genes. This information can be utilized to make diagnostic reagents specific for the expression products of the differentially expressed genes. It can also be used in diagnostic and prognostic methods which will help clinicians in planning appropriate treatment regimes for cancers, especially of the breast or colon.

Some of the polynucleotides disclosed herein represent novel genes which are differentially expressed between non-metastatic cancer cells and cancer cells which have a potential to metastasize. SEQ ID NOS:1-63 represent novel metastatic marker genes (Table 1). SEQ ID NOS:64-85 represent known genes which have been found to be differentially expressed in metastatic relative to non-metastatic cancer cells (Table 2). Some of the metastatic marker genes disclosed herein are expressed in

metastatic cells relative to non-metastatic cells, particularly in breast cancer cells which metastasize to bone and lung (SEQ ID NOS:1, 5, 11, 18, 20, 22, 24, 30, 33, 35, 36, 38, 45, 52, 58, 65, 66, 70, 74, 76, and 80). One metastatic marker gene (SEQ ID NO:56) is expressed in non-metastatic breast cancer cells and in colon cancer cells with low metastatic potential. Other metastatic marker genes are expressed in metastatic cancer cells, particularly in breast cancer cells which metastasize only to lung (SEQ ID NOS:2, 4, 9, 13, 14, 19, 26, 29, 39-41, 48, 55, 57, 60, 63, 64, 72, 73, 82, and 83). Still other metastatic marker genes (SEQ ID NOS:3, 7, 8, 10, 12, 15-17, 21, 23, 28, 31, 34, 37, 42-44, 46, 47, 49, 61, 62, 67, 68, 75, 77-79, 81, 84, and 85) are expressed in cancer cells which do not typically metastasize, particularly in breast cancer cells. Identification of these relationships and markers permits the formulation of reagents and methods as further described below. Other metastatic marker genes, such as those which comprise a nucleotide sequence shown in SEQ ID NOS:6, 27, 32, and 54, can be used to identify cancerous tissue, particularly breast cancer tissue.

Sequences of metastatic marker genes are disclosed in SEQ ID NOS:1-85. Metastatic marker proteins can be made by expression of the disclosed polynucleotide molecules. Amino acid sequences encoded by novel polynucleotides of the invention can be predicted by running a translation program for each of three reading frames for a disclosed sequence and its complement. Complete polynucleotide sequences can be obtained by chromosome walking, screening of libraries for overlapping clones, 5' RACE, or other techniques well known in the art.

Reference to metastatic marker nucleotide or amino acid sequences includes variants which have similar expression patterns in metastatic relative to non-metastatic cells, as described below. Metastatic marker polypeptides can differ in length from full-length metastatic marker proteins and contain at least 6, 8, 10, 12, 15, 18, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 120, 140, 160, 180, or 200 or more contiguous amino acids of a metastatic marker protein.

Variants of marker proteins and polypeptides can also occur. Metastatic marker protein or polypeptide variants can be naturally or non-naturally occurring. Naturally occurring metastatic marker protein or polypeptide variants are found in

humans or other species and comprise amino acid sequences which are substantially identical to the proteins encoded by genes corresponding to the nucleotide sequences shown in SEQ ID NOS:1-85 or their complements. Non-naturally occurring metastatic marker protein or polypeptide variants which retain substantially the same differential
5 expression patterns in metastatic relative to non-metastatic cancer cells as naturally occurring metastatic marker protein or polypeptide variants are also included here. Preferably, naturally or non-naturally occurring metastatic marker protein or polypeptide variants have amino acid sequences which are at least 85%, 90%, or 95% identical to amino acid sequences encoded by the nucleotide sequences shown in SEQ
10 ID NOS:1-85. More preferably, the molecules are at least 98% or 99% identical. Percent sequence identity between a wild-type protein or polypeptide and a variant is determined by aligning the wild-type protein or polypeptide with the variant to obtain the greatest number of amino acid matches, as is known in the art, counting the number of amino acid matches between the wild-type and the variant, and dividing the total
15 number of matches by the total number of amino acid residues of the wild-type sequence.

Preferably, amino acid changes in metastatic marker protein or polypeptide variants are conservative amino acid changes, *i.e.*, substitutions of similarly charged or uncharged amino acids. A conservative amino acid change involves
20 substitution of one of a family of amino acids which are related in their side chains. Naturally occurring amino acids are generally divided into four families: acidic (aspartate, glutamate), basic (lysine, arginine, histidine), non-polar (alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), and uncharged polar (glycine, asparagine, glutamine, cystine, serine, threonine, tyrosine) amino acids.
25 Phenylalanine, tryptophan, and tyrosine are sometimes classified jointly as aromatic amino acids.

It is reasonable to expect that an isolated replacement of a leucine with an isoleucine or valine, an aspartate with a glutamate, a threonine with a serine, or a similar replacement of an amino acid with a structurally related amino acid will not
30 have a major effect on the biological properties of the resulting metastatic marker

protein or polypeptide variant. Properties and functions of metastatic marker protein or polypeptide variants are of the same type as a metastatic marker protein or polypeptide comprising amino acid sequences encoded by the nucleotide sequences shown in SEQ ID NOS:1-85, although the properties and functions of variants can differ in degree.

5 Whether an amino acid change results in a metastatic marker protein or polypeptide variant with the appropriate differential expression pattern can readily be determined. For example, nucleotide probes can be selected from the marker gene sequences disclosed herein and used to detect marker gene mRNA in Northern blots or in tissue sections, as is known in the art. Alternatively, antibodies which specifically bind to

10 protein products of metastatic marker genes can be used to detect expression of metastatic marker proteins.

Metastatic marker variants include glycosylated forms, aggregative conjugates with other molecules, and covalent conjugates with unrelated chemical moieties. Metastatic marker variants also include allelic variants, species variants, and

15 muteins. Truncations or deletions of regions which do not affect the differential expression of metastatic marker genes are also metastatic marker variants. Covalent variants can be prepared by linking functionalities to groups which are found in the amino acid chain or at the N- or C-terminal residue, as is known in the art.

Full-length metastatic marker proteins can be extracted, using standard

20 biochemical methods, from metastatic marker protein-producing human cells, such as metastatic breast or colon cancer cells. An isolated and purified metastatic marker protein or polypeptide is separated from other compounds which normally associate with a metastatic marker protein or polypeptide in a cell, such as certain proteins, carbohydrates, lipids, or subcellular organelles. A preparation of isolated and purified

25 metastatic marker proteins or polypeptides is at least 80% pure; preferably, the preparations are 90%, 95%, or 99% pure.

Metastatic marker proteins and polypeptides can also be produced by recombinant DNA methods or by synthetic chemical methods. For production of recombinant metastatic marker proteins or polypeptides, coding sequences selected

30 from the nucleotide sequences shown in SEQ ID NOS:1-85, or variants of those

sequences which encode metastatic marker proteins, can be expressed in known prokaryotic or eukaryotic expression systems (see below). Bacterial, yeast, insect, or mammalian expression systems can be used, as is known in the art.

Alternatively, synthetic chemical methods, such as solid phase peptide synthesis, can be used to synthesize a metastatic marker protein or polypeptide. General means for the production of peptides, analogs or derivatives are outlined in CHEMISTRY AND BIOCHEMISTRY OF AMINO ACIDS, PEPTIDES, AND PROTEINS -- A SURVEY OF RECENT DEVELOPMENTS, Weinstein, B. ed., Marcell Dekker, Inc., publ., New York (1983). Moreover, substitution of D-amino acids for the normal L-stereoisomer can be carried out to increase the half-life of the molecule. Metastatic marker variants can be similarly produced.

Non-naturally occurring fusion proteins comprising at least 6, 8, 10, 12, 15, 18, 20, 25, 30, 35, 40, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 120, 140, 160, 180, or 200 or more contiguous metastatic marker amino acids can also be constructed. Human metastatic marker fusion proteins are useful for generating antibodies against metastatic marker amino acid sequences and for use in various assay systems. For example, metastatic marker fusion proteins can be used to identify proteins which interact with metastatic marker proteins and influence their functions. Physical methods, such as protein affinity chromatography, or library-based assays for protein-protein interactions, such as the yeast two-hybrid or phage display systems, can also be used for this purpose. Such methods are well known in the art and can also be used as drug screens.

A metastatic marker fusion protein comprises two protein segments fused together by means of a peptide bond. The first protein segment comprises at least 6, 8, 10, 12, 15, 18, 20, 25, 30, 35, 40, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 120, 140, 160, 180, or 200 or more contiguous amino acids of a metastatic marker protein. The amino acids can be selected from the amino acid sequences encoded by the nucleotide sequences shown in SEQ ID NOS:1-85 or from variants of those sequences, such as those described above. The first protein segment can also comprise a full-length metastatic marker protein.

The second protein segment can be a full-length protein or a protein fragment or polypeptide. The fusion protein can be labeled with a detectable marker, as is known in the art, such as a radioactive, fluorescent, chemiluminescent, or biotinylated marker. The second protein segment can be an enzyme which will generate a detectable
5 product, such as β -galactosidase. The first protein segment can be N-terminal or C-terminal, as is convenient.

Techniques for making fusion proteins, either recombinantly or by covalently linking two protein segments, are also well known. Recombinant DNA methods can be used to prepare metastatic marker fusion proteins, for example, by
10 making a DNA construct which comprises coding sequences selected from SEQ ID NOS:1-85 in proper reading frame with nucleotides encoding the second protein segment and expressing the DNA construct in a host cell, as described below.

Isolated and purified metastatic marker proteins, polypeptides, variants, or fusion proteins can be used as immunogens, to obtain preparations of antibodies
15 which specifically bind to a metastatic marker protein. The antibodies can be used, *inter alia*, to detect wild-type metastatic marker proteins in human tissue and fractions thereof. The antibodies can also be used to detect the presence of mutations in metastatic marker genes which result in under- or over-expression of a metastatic marker protein or in expression of a metastatic marker protein with altered size or
20 electrophoretic mobility.

Preparations of polyclonal or monoclonal antibodies can be made using standard methods. Single-chain antibodies can also be prepared. Single-chain antibodies which specifically bind to metastatic marker proteins, polypeptides, variants, or fusion proteins can be isolated, for example, from single-chain immunoglobulin
25 display libraries, as is known in the art. The library is "panned" against metastatic marker protein amino acid sequences, and a number of single chain antibodies which bind with high-affinity to different epitopes of metastatic marker proteins can be isolated. Hayashi *et al.*, 1995, *Gene* 160:129-30. Single-chain antibodies can also be constructed using a DNA amplification method, such as the polymerase chain reaction

(PCR), using hybridoma cDNA as a template. Thirion *et al.*, 1996, *Eur. J. Cancer Prev.* 5:507-11.

Single-chain antibodies can be mono- or bispecific, and can be bivalent or tetravalent. Construction of tetravalent, bispecific single-chain antibodies is taught in
5 Coloma and Morrison, 1997, *Nat. Biotechnol.* 15:159-63. Construction of bivalent, bispecific single-chain antibodies is taught in Mallender and Voss, 1994, *J. Biol. Chem.* 269:199-206.

A nucleotide sequence encoding the single-chain antibody can be constructed using manual or automated nucleotide synthesis, cloned into DNA
10 expression constructs using standard recombinant DNA methods, and introduced into cells which express the coding sequence, as described below. Alternatively, single-chain antibodies can be produced directly using, for example, filamentous phage technology. Verhaar *et al.*, 1995, *Int. J. Cancer* 61:497-501; Nicholls *et al.*, 1993, *J. Immunol. Meth.* 165:81-91.

15 Metastatic marker-specific antibodies specifically bind to epitopes present in a full-length metastatic marker protein having an amino acid sequence encoded by a nucleotide sequence shown in SEQ ID NOS:1-85, to metastatic marker polypeptides, or to metastatic marker variants, either alone or as part of a fusion protein. Preferably, metastatic marker epitopes are not present in other human proteins.
20 Typically, at least 6, 8, 10, or 12 contiguous amino acids are required to form an epitope. However, epitopes which involve non-contiguous amino acids may require more, *e.g.*, at least 15, 25, or 50 amino acids.

Antibodies which specifically bind to metastatic marker proteins, polypeptides, fusion proteins, or variants provide a detection signal at least 5-, 10-, or
25 20-fold higher than a detection signal provided with other proteins when used in Western blots or other immunochemical assays. Preferably, antibodies which specifically bind to metastatic marker epitopes do not detect other proteins in immunochemical assays and can immunoprecipitate a metastatic marker protein, polypeptide, fusion protein, or variant from solution.

Antibodies can be purified by methods well known in the art. Preferably, the antibodies are affinity purified, by passing the antibodies over a column to which a metastatic marker protein, polypeptide, variant, or fusion protein is bound. The bound antibodies can then be eluted from the column, for example, using a buffer
5 with a high salt concentration.

Subgenomic polynucleotides contain less than a whole chromosome. Preferably, the polynucleotides are intron-free. In a preferred embodiment, the polynucleotide molecules comprise a contiguous sequence of 10, 11, 12, 15, 20, 25, 30, 32, 35, 40, 45, 50, 60, 70, 74, 80, 90, 100, 125, 150, 154, 175, 182, 200, 243, or 268
10 nucleotides selected from SEQ ID NOS:1-85 or the complements thereof. The complement of a nucleotide sequence shown in SEQ ID NOS:1-85 is a contiguous nucleotide sequence which forms Watson-Crick base pairs with a contiguous nucleotide sequence shown in SEQ ID NOS:1-85. The complement of a nucleotide sequence shown in SEQ ID NOS:1-85 (the antisense strand) is also a subgenomic polynucleotide.
15 and can be used provide marker protein antisense oligonucleotides. Double-stranded polynucleotides which comprise one of the nucleotide sequences shown in SEQ ID NOS:1-85 are also subgenomic polynucleotides. Metastatic marker protein subgenomic polynucleotides also include polynucleotides which encode metastatic marker protein-specific single-chain antibodies and ribozymes, or fusion proteins
20 comprising metastatic marker protein amino acid sequences.

Degenerate nucleotide sequences encoding amino acid sequences of metastatic marker protein and or variants, as well as homologous nucleotide sequences which are at least 85%, 90%, 95%, 98%, or 99% identical to the nucleotide sequences shown in SEQ ID NOS:1-85, are also metastatic marker subgenomic polynucleotides.
25 Typically, homologous metastatic marker subgenomic polynucleotide sequences can be confirmed by hybridization under stringent conditions, as is known in the art. Percent sequence identity between wild-type and homologous variant sequences is determined by aligning the wild-type polynucleotide with the variant to obtain the greatest number of nucleotide matches, as is known in the art, counting the number of nucleotide
30 matches between the wild-type and the variant, and dividing the total number of

matches by the total number of nucleotides of the wild-type sequence. A preferred algorithm for calculating percent identity is the Smith-Waterman homology search algorithm as implemented in MPSRCH program (Oxford Molecular) using an affine gap search with the following search parameters: gap open penalty of 10, and gap
5 extension penalty of 1.

Metastatic marker subgenomic polynucleotides can be isolated and purified free from other nucleotide sequences using standard nucleic acid purification techniques. For example, restriction enzymes and probes can be used to isolate polynucleotide fragments which comprise nucleotide sequences encoding a metastatic
10 marker protein. Isolated and purified subgenomic polynucleotides are in preparations which are free or at least 90% free of other molecules.

Complementary DNA molecules which encode metastatic marker proteins can be made using reverse transcriptase, with metastatic marker mRNA as a template. The polymerase chain reaction (PCR) or other amplification techniques can
15 be used to obtain metastatic marker subgenomic polynucleotides, using either human genomic DNA or cDNA as a template, as is known in the art. Alternatively, synthetic chemistry techniques can be used to synthesize metastatic marker subgenomic polynucleotides which comprise coding sequences for regions of metastatic marker proteins, single-chain antibodies, or ribozymes, or which comprise antisense
20 oligonucleotides. The degeneracy of the genetic code allows alternate nucleotide sequences to be synthesized which will encode a metastatic marker protein comprising amino acid sequences encoded by the nucleotide sequences shown in SEQ ID NOS:1-85.

Purified and isolated metastatic marker subgenomic polynucleotides can
25 be used as primers to obtain additional copies of the polynucleotides or as probes for identifying wild-type and mutant metastatic marker protein coding sequences. Metastatic marker subgenomic polynucleotides can be used to express metastatic marker mRNA, protein, polypeptides, or fusion proteins and to generate metastatic marker antisense oligonucleotides and ribozymes.

A metastatic marker subgenomic polynucleotide comprising metastatic marker protein coding sequences can be used in an expression construct. Preferably, the metastatic marker subgenomic polynucleotide is inserted into an expression plasmid (for example, the Ecdyson system, pIND, In Vitro Gene). Metastatic marker
5 subgenomic polynucleotides can be propagated in vectors and cell lines using techniques well known in the art. Metastatic marker subgenomic polynucleotides can be on linear or circular molecules. They can be on autonomously replicating molecules or on molecules without replication sequences. They can be regulated by their own or by other regulatory sequences, as are known in the art.

10 A host cell comprising a metastatic marker expression construct can then be used to express all or a portion of a metastatic marker protein. Host cells comprising metastatic marker expression constructs can be prokaryotic or eukaryotic. A variety of host cells are available for use in bacterial, yeast, insect, and human expression systems and can be used to express or to propagate metastatic marker
15 expression constructs (see below). Expression constructs can be introduced into host cells using any technique known in the art. These techniques include transferrin-polycation-mediated DNA transfer, transfection with naked or encapsulated nucleic acids, liposome-mediated cellular fusion, intracellular transportation of DNA-coated latex beads, protoplast fusion, viral infection, electroporation, and calcium phosphate-mediated transfection.
20

A metastatic marker expression construct comprises a promoter which is functional in a chosen host cell. The skilled artisan can readily select an appropriate promoter from the large number of cell type-specific promoters known and used in the art. The expression construct can also contain a transcription terminator which is
25 functional in the host cell. The expression construct comprises a polynucleotide segment which encodes all or a portion of the metastatic marker protein, variant, fusion protein, antibody, or ribozyme. The polynucleotide segment is located downstream from the promoter. Transcription of the polynucleotide segment initiates at the promoter. The expression construct can be linear or circular and can contain sequences,
30 if desired, for autonomous replication.

Bacterial systems for expressing metastatic marker expression constructs include those described in Chang *et al.*, *Nature* (1978) 275: 615. Goeddel *et al.*, *Nature* (1979) 281: 544, Goeddel *et al.*, *Nucleic Acids Res.* (1980) 8: 4057, EP 36,776, U.S. 4,551,433, deBoer *et al.*, *Proc. Nat'l Acad. Sci. USA* (1983) 80: 21-25, and Siebenlist *et al.*, *Cell* (1980) 20: 269.

Expression systems in yeast include those described in Hinnen *et al.*, *Proc. Nat'l Acad. Sci. USA* (1978) 75: 1929; Ito *et al.*, *J. Bacteriol.* (1983) 153: 163; Kurtz *et al.*, *Mol. Cell. Biol.* (1986) 5: 142; Kunze *et al.*, *J. Basic Microbiol.* (1985) 25: 141; Gleeson *et al.*, *J. Gen. Microbiol.* (1986) 132: 3459, Roggenkamp *et al.*, *Mol. Gen. Genet.* (1986) 202 :302; Das *et al.*, *J. Bacteriol.* (1984) 158: 1165; De Louvencourt *et al.*, *J. Bacteriol.* (1983) 154: 737, Van den Berg *et al.*, *Bio/Technology* (1990) 8: 135; Kunze *et al.*, *J. Basic Microbiol.* (1985) 25: 141; Cregg *et al.*, *Mol. Cell. Biol.* (1985) 5: 3376, U.S. 4,837,148, US 4,929,555; Beach and Nurse, *Nature* (1981) 300: 706; Davidow *et al.*, *Curr. Genet.* (1985) 10: 380, Gaillardin *et al.*, *Curr. Genet.* (1985) 10: 49, Ballance *et al.*, *Biochem. Biophys. Res. Commun.* (1983) 112: 284-289; Tilburn *et al.*, *Gene* (1983) 26: 205-221, Yelton *et al.*, *Proc. Nat'l Acad. Sci. USA* (1984) 81: 1470-1474, Kelly and Hynes, *EMBO J.* (1985) 4: 475479; EP 244,234, and WO 91/00357.

Expression of metastatic marker expression constructs in insects can be carried out as described in U.S. 4,745,051, Friesen *et al.* (1986) "The Regulation of Baculovirus Gene Expression" in: THE MOLECULAR BIOLOGY OF BACULOVIRUSES (W. Doerfler, ed.), EP 127,839, EP 155,476, and Vlak *et al.*, *J. Gen. Virol.* (1988) 69: 765-776, Miller *et al.*, *Ann. Rev. Microbiol.* (1988) 42: 177, Carbonell *et al.*, *Gene* (1988) 73: 409, Maeda *et al.*, *Nature* (1985) 315: 592-594, Lebacqz-Verheyden *et al.*, *Mol. Cell. Biol.* (1988) 8: 3129; Smith *et al.*, *Proc. Nat'l Acad. Sci. USA* (1985) 82: 8404, Miyajima *et al.*, *Gene* (1987) 58: 273; and Martin *et al.*, *DNA* (1988) 7:99. Numerous baculoviral strains and variants and corresponding permissive insect host cells from hosts are described in Luckow *et al.*, *Bio/Technology* (1988) 6: 47-55, Miller *et al.*, in GENETIC ENGINEERING (Setlow, J.K. *et al.* eds.), Vol. 8 (Plenum Publishing, 1986), pp. 277-279, and Maeda *et al.*, *Nature*, (1985) 315: 592-594.

Mammalian expression of metastatic marker expression constructs can be achieved as described in Dijkema *et al.*, *EMBO J.* (1985) 4: 761, Gorman *et al.*, *Proc. Nat'l Acad. Sci. USA* (1982b) 79: 6777, Boshart *et al.*, *Cell* (1985) 41: 521 and U.S. 4,399,216. Other features of mammalian expression of metastatic marker
5 expression constructs can be facilitated as described in Ham and Wallace, *Meth. Enz.* (1979) 58: 44, Barnes and Sato, *Anal. Biochem.* (1980) 102: 255, U.S. 4,767,704, US 4,657,866, US 4,927,762, US 4,560,655, WO 90/103430, WO 87/00195, and U.S. RE 30,985.

Subgenomic polynucleotides of the invention can also be used in gene
10 delivery vehicles, for the purpose of delivering a metastatic marker mRNA or oligonucleotide (either with the sequence of native metastatic marker mRNA or its complement), full-length metastatic marker protein, metastatic marker fusion protein, metastatic marker polypeptide, or metastatic marker-specific ribozyme or single-chain antibody, into a cell preferably a eukaryotic cell. According to the present invention, a
15 gene delivery vehicle can be, for example, naked plasmid DNA, a viral expression vector comprising a metastatic marker subgenomic polynucleotide, or a metastatic marker subgenomic polynucleotide in conjunction with a liposome or a condensing agent.

In one embodiment of the invention, the gene delivery vehicle comprises
20 a promoter and a metastatic marker subgenomic polynucleotide. Preferred promoters are tissue-specific promoters and promoters which are activated by cellular proliferation, such as the thymidine kinase and thymidylate synthase promoters. Other preferred promoters include promoters which are activatable by infection with a virus, such as the α - and β -interferon promoters, and promoters which are activatable by a
25 hormone, such as estrogen. Other promoters which can be used include the Moloney virus LTR, the CMV promoter, and the mouse albumin promoter.

A metastatic marker gene delivery vehicle can comprise viral sequences such as a viral origin of replication or packaging signal. These viral sequences can be selected from viruses such as astrovirus, coronavirus, orthomyxovirus, papovavirus,
30 paramyxovirus, parvovirus, picornavirus, poxvirus, retrovirus, togavirus or adenovirus.

In a preferred embodiment, the metastatic marker gene delivery vehicle is a recombinant retroviral vector. Recombinant retroviruses and various uses thereof have been described in numerous references including, for example, Mann *et al.*, *Cell* 33:153, 1983, Cane and Mulligan, *Proc. Nat'l Acad. Sci. USA* 81:6349, 1984, Miller *et al.*, *Human Gene Therapy* 1:5-14, 1990, U.S. Patent Nos. 4,405,712, 4,861,719, and 4,980,289, and PCT Application Nos. WO 89/02,468, WO 89/05,349, and WO 90/02,806. Numerous retroviral gene delivery vehicles can be utilized in the present invention, including for example those described in EP 0,415,731; WO 90/07936; WO 94/03622; WO 93/25698; WO 93/25234; U.S. Patent No. 5,219,740; WO 9311230; 10 WO 9310218; Vile and Hart, *Cancer Res.* 53:3860-3864, 1993; Vile and Hart, *Cancer Res.* 53:962-967, 1993; Ram *et al.*, *Cancer Res.* 53:83-88, 1993; Takamiya *et al.*, *J. Neurosci. Res.* 33:493-503, 1992; Baba *et al.*, *J. Neurosurg.* 79:729-735, 1993 (U.S. Patent No. 4,777,127, GB 2,200,651, EP 0,345,242 and WO91/02805).

Particularly preferred retroviruses are derived from retroviruses which 15 include avian leukosis virus (ATCC Nos. VR-535 and VR-247), bovine leukemia virus (VR-1315), murine leukemia virus (MLV), mink-cell focus-inducing virus (Koch *et al.*, *J. Vir.* 49:828, 1984; and Oliff *et al.*, *J. Vir.* 48:542, 1983), murine sarcoma virus (ATCC Nos. VR-844, 45010 and 45016), reticuloendotheliosis virus (ATCC Nos VR-994, VR-770 and 45011), Rous sarcoma virus, Mason-Pfizer monkey virus, baboon 20 endogenous virus, endogenous feline retrovirus (*e.g.*, RD114), and mouse or rat gL30 sequences used as a retroviral vector. Particularly preferred strains of MLV from which recombinant retroviruses can be generated include 4070A and 1504A (Hartley and Rowe, *J. Vir.* 19:19, 1976), Abelson (ATCC No. VR-999), Friend (ATCC No. VR-245), Graffi (Ru *et al.*, *J. Vir.* 67:4722, 1993; and Yantchev *Neoplasma* 26:397, 1979), 25 Gross (ATCC No. VR-590), Kirsten (Albino *et al.*, *J. Exp. Med.* 164:1710, 1986), Harvey sarcoma virus (Manly *et al.*, *J. Vir.* 62:3540, 1988; and Albino *et al.*, *J. Exp. Med.* 164:1710, 1986) and Rauscher (ATCC No. VR-998), and Moloney MLV (ATCC No. VR-190). A particularly preferred non-mouse retrovirus is Rous sarcoma virus. Preferred Rous sarcoma viruses include Bratislava (Manly *et al.*, *J. Vir.* 62:3540, 1988; 30 and Albino *et al.*, *J. Exp. Med.* 164:1710, 1986), Bryan high titer (*e.g.*, ATCC Nos. VR-

334, VR-657, VR-726, VR-659, and VR-728), Bryan standard (ATCC No. VR-140), Carr-Zilber (Adighitov *et al.*, *Neoplasma* 27:159, 1980), Engelbreth-Holm (Laurent *et al.*, *Biochem Biophys Acta* 908:241, 1987), Harris, Prague (*e.g.*, ATCC Nos. VR-772, and 45033), and Schmidt-Ruppin (*e.g.*, ATCC Nos. VR-724, VR-725, VR-354) viruses.

5 Any of the above retroviruses can be readily utilized in order to assemble or construct retroviral metastatic marker gene delivery vehicles given the disclosure provided herein and standard recombinant techniques (*e.g.*, Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, 2d ed., Cold Spring Harbor Laboratory Press, 1989, and Kunkle, *PNAS* 82:488, 1985) known in the art. Portions of retroviral *Metastatic*
10 *marker* expression vectors can be derived from different retroviruses. For example, retrovector LTRs can be derived from a murine sarcoma virus, a tRNA binding site from a Rous sarcoma virus, a packaging signal from a murine leukemia virus, and an origin of second strand synthesis from an avian leukosis virus. These recombinant retroviral vectors can be used to generate transduction competent retroviral vector
15 particles by introducing them into appropriate packaging cell lines (*see* Serial No. 07/800,921, filed November 29, 1991). Recombinant retroviruses can be produced which direct the site-specific integration of the recombinant retroviral genome into specific regions of the host cell DNA. Such site-specific integration can be mediated by a chimeric integrase incorporated into the retroviral particle (*see* Serial No. 08/445,466
20 filed May 22, 1995). It is preferable that the recombinant viral gene delivery vehicle is a replication-defective recombinant virus.

Packaging cell lines suitable for use with the above-described retroviral gene delivery vehicles can be readily prepared (*see* Serial No. 08/240,030, filed May 9, 1994; *see also* WO 92/05266) and used to create producer cell lines (also termed vector
25 cell lines or "VCLs") for production of recombinant viral particles. In particularly preferred embodiments of the present invention, packaging cell lines are made from human (*e.g.*, HIT1080 cells) or mink parent cell lines, thereby allowing production of recombinant retroviral gene delivery vehicles which are capable of surviving inactivation in human serum. The construction of recombinant retroviral gene delivery
30 vehicles is described in detail in WO 91/02805. These recombinant retroviral gene

delivery vehicles can be used to generate transduction competent retroviral particles by introducing them into appropriate packaging cell lines (*see* Serial No. 07/800,921). Similarly, adenovirus gene delivery vehicles can also be readily prepared and utilized given the disclosure provided herein (*see also* Berkner, *Biotechniques* 6:616-627, 1988, 5 and Rosenfeld *et al.*, *Science* 252:431-434, 1991, WO 93/07283, WO 93/06223, and WO 93/07282).

A metastatic marker gene delivery vehicle can also be a recombinant adenoviral gene delivery vehicle. Such vehicles can be readily prepared and utilized given the disclosure provided herein (*see* Berkner, *Biotechniques* 6:616, 1988, and 10 Rosenfeld *et al.*, *Science* 252:431, 1991, WO 93/07283, WO 93/06223, and WO 93/07282). Adeno-associated viral metastatic marker gene delivery vehicles can also be constructed and used to deliver metastatic marker amino acids or nucleotides. The use of adeno-associated viral gene delivery vehicles *in vitro* is described in Chatterjee *et al.*, *Science* 258: 1485-1488 (1992), Walsh *et al.*, *Proc. Nat'l Acad. Sci.* 89: 7257-7261 15 (1992), Walsh *et al.*, *J. Clin. Invest.* 94: 1440-1448 (1994), Flotte *et al.*, *J. Biol. Chem.* 268: 3781-3790 (1993), Ponnazhagan *et al.*, *J. Exp. Med.* 179: 733-738 (1994), Miller *et al.*, *Proc. Nat'l Acad. Sci.* 91: 10183-10187 (1994), Einerhand *et al.*, *Gene Ther.* 2: 336-343 (1995), Luo *et al.*, *Exp. Hematol.* 23: 1261-1267 (1995), and Zhou *et al.*, *Gene Therapy* 3: 223-229 (1996). *In vivo* use of these vehicles is described in Flotte *et al.*, 20 *Proc. Nat'l Acad. Sci.* 90: 10613-10617 (1993), and Kaplitt *et al.*, *Nature Genet.* 8:148-153 (1994).

In another embodiment of the invention, a metastatic marker gene delivery vehicle is derived from a togavirus. Preferred togaviruses include alphaviruses, in particular those described in U.S. Serial No. 08/405,627, filed March 15, 1995, WO 25 95/07994. Alpha viruses, including Sindbis and ELVS viruses can be gene delivery vehicles for metastatic marker polynucleotides. Alpha viruses are described in WO 94/21792, WO 92/10578 and WO 95/07994. Several different alphavirus gene delivery vehicle systems can be constructed and used to deliver metastatic marker subgenomic polynucleotides to a cell according to the present invention. Representative examples 30 of such systems include those described in U.S. Patents 5,091,309 and 5,217,879.

Particularly preferred alphavirus gene delivery vehicles for use in the present invention include those which are described in WO 95/07994, and U.S. Serial No. 08/405,627.

Preferably, the recombinant viral vehicle is a recombinant alphavirus viral vehicle based on a Sindbis virus. Sindbis constructs, as well as numerous similar
5 constructs, can be readily prepared essentially as described in U.S. Serial No. 08/198,450. Sindbis viral gene delivery vehicles typically comprise a 5' sequence capable of initiating Sindbis virus transcription, a nucleotide sequence encoding Sindbis non-structural proteins, a viral junction region inactivated so as to prevent subgenomic fragment transcription, and a Sindbis RNA polymerase recognition sequence.
10 Optionally, the viral junction region can be modified so that subgenomic polynucleotide transcription is reduced, increased, or maintained. As will be appreciated by those in the art, corresponding regions from other alphaviruses can be used in place of those described above.

The viral junction region of an alphavirus-derived gene delivery vehicle
15 can comprise a first viral junction region which has been inactivated in order to prevent transcription of the subgenomic polynucleotide and a second viral junction region which has been modified such that subgenomic polynucleotide transcription is reduced. An alphavirus-derived vehicle can also include a 5' promoter capable of initiating synthesis of viral RNA from cDNA and a 3' sequence which controls transcription
20 termination.

Other recombinant togaviral gene delivery vehicles which can be utilized in the present invention include those derived from Semliki Forest virus (ATCC VR-67; ATCC VR-1247), Middleberg virus (ATCC VR-370), Ross River virus (ATCC VR-373; ATCC VR-1246), Venezuelan equine encephalitis virus (ATCC VR923; ATCC
25 VR-1250; ATCC VR-1249; ATCC VR-532), and those described in U.S. Patents 5,091,309 and 5,217,879 and in WO 92/10578. The Sindbis vehicles described above, as well as numerous similar constructs, can be readily prepared essentially as described in U.S. Serial No. 08/198,450.

Other viral gene delivery vehicles suitable for use in the present
30 invention include, for example, those derived from poliovirus (Evans *et al.*, *Nature*

339:385, 1989, and Sabin *et al.*, *J. Biol. Standardization* 1:115, 1973) (ATCC VR-58); rhinovirus (Arnold *et al.*, *J. Cell. Biochem.* L401, 1990) (ATCC VR-1110); pox viruses, such as canary pox virus or vaccinia virus (Fisher-Hoch *et al.*, *PNAS* 86:317, 1989; Flexner *et al.*, *Ann. N.Y. Acad. Sci.* 569:86, 1989; Flexner *et al.*, *Vaccine* 8:17, 1990; U.S. 4,603,112 and U.S. 4,769,330; WO 89/01973) (ATCC VR-111; ATCC VR-2010); SV40 (Mulligan *et al.*, *Nature* 277:108, 1979) (ATCC VR-305), (Madzak *et al.*, *J. Gen. Vir.* 73:1533, 1992); influenza virus (Luytjes *et al.*, *Cell* 59:1107, 1989; McMichael *et al.*, *The New England Journal of Medicine* 309:13, 1983; and Yap *et al.*, *Nature* 273:238, 1978) (ATCC VR-797); parvovirus such as adeno-associated virus (Samulski *et al.*, *J. Vir.* 63:3822, 1989, and Mendelson *et al.*, *Virology* 166:154, 1988) (ATCC VR-645); herpes simplex virus (Kit *et al.*, *Adv. Exp. Med. Biol.* 215:219, 1989) (ATCC VR-977; ATCC VR-260); *Nature* 277: 108, 1979); human immunodeficiency virus (EPO 386,882, Buchschacher *et al.*, *J. Vir.* 66:2731, 1992); measles virus (EPO 440,219) (ATCC VR-24); A (ATCC VR-67; ATCC VR-1247), Aura (ATCC VR-368), Bebaru virus (ATCC VR-600; ATCC VR-1240), Cabassou (ATCC VR-922), Chikungunya virus (ATCC VR-64; ATCC VR-1241), Fort Morgan (ATCC VR-924), Getah virus (ATCC VR-369; ATCC VR-1243), Kyzylagach (ATCC VR-927), Mayaro (ATCC VR-66), Mucambo virus (ATCC VR-580; ATCC VR-1244), Ndumu (ATCC VR-371), Pixuna virus (ATCC VR-372; ATCC VR-1245), Tonate (ATCC VR-925), Trinita (ATCC VR-469), Una (ATCC VR-374), Whataroa (ATCC VR-926), Y-62-33 (ATCC VR-375), O'Nyong virus, Eastern encephalitis virus (ATCC VR-65; ATCC VR-1242), Western encephalitis virus (ATCC VR-70; ATCC VR-1251; ATCC VR-622; ATCC VR-1252), and coronavirus (Hamre *et al.*, *Proc. Soc. Exp. Biol. Med.* 121:190, 1966) (ATCC VR-740).

25 A subgenomic metastatic marker polynucleotide of the invention can also be combined with a condensing agent to form a gene delivery vehicle. In a preferred embodiment, the condensing agent is a polycation, such as polylysine, polyarginine, polyornithine, protamine, spermine, spermidine, and putrescine. Many suitable methods for making such linkages are known in the art (see, for example, Serial
30 No. 08/366,787, filed December 30, 1994).

In an alternative embodiment, a metastatic marker subgenomic polynucleotide is associated with a liposome to form a gene delivery vehicle. Liposomes are small, lipid vesicles comprised of an aqueous compartment enclosed by a lipid bilayer, typically spherical or slightly elongated structures several hundred
5 Angstroms in diameter. Under appropriate conditions, a liposome can fuse with the plasma membrane of a cell or with the membrane of an endocytic vesicle within a cell which has internalized the liposome, thereby releasing its contents into the cytoplasm. Prior to interaction with the surface of a cell, however, the liposome membrane acts as a relatively impermeable barrier which sequesters and protects its contents, for example,
10 from degradative enzymes. Additionally, because a liposome is a synthetic structure, specially designed liposomes can be produced which incorporate desirable features. See Stryer, *Biochemistry*, pp. 236-240, 1975 (W.H. Freeman, San Francisco, CA); Szoka *et al.*, *Biochim. Biophys. Acta* 600:1, 1980; Bayer *et al.*, *Biochim. Biophys. Acta* 550:464, 1979; Rivnay *et al.*, *Meth. Enzymol.* 149:119, 1987; Wang *et al.*, *PNAS* 84:
15 7851, 1987. Plant *et al.*, *Anal. Biochem.* 176:420, 1989, and U.S. Patent 4,762,915. Liposomes can encapsulate a variety of nucleic acid molecules including DNA, RNA, plasmids, and expression constructs comprising metastatic marker subgenomic polynucleotides such those disclosed in the present invention.

Liposomal preparations for use in the present invention include cationic
20 (positively charged), anionic (negatively charged) and neutral preparations. Cationic liposomes have been shown to mediate intracellular delivery of plasmid DNA (Felgner *et al.*, *Proc. Nat'l Acad. Sci. USA* 84:7413-7416, 1987), mRNA (Malone *et al.*, *Proc. Nat'l Acad. Sci. USA* 86:6077-6081, 1989), and purified transcription factors (Debs *et al.*, *J. Biol. Chem.* 265:10189-10192, 1990), in functional form. Cationic liposomes are
25 readily available. For example, N[1-(2,3-dioleoyloxy)propyl]-N,N,N-triethylammonium (DOTMA) liposomes are available under the trademark Lipofectin, from GIBCO BRL, Grand Island, NY. See also Felgner *et al.*, *Proc. Nat'l Acad. Sci. USA* 91: 5148-5152, 1994. Other commercially available liposomes include Transfectace (DDAB/DOPE) and DOTAP/DOPE (Boehringer). Other cationic liposomes can be
30 prepared from readily available materials using techniques well known in the art. See,

e.g., Szoka *et al.*, *Proc. Nat'l Acad. Sci. USA* 75:4194-4198, 1978; and WO 90/11092 for descriptions of the synthesis of DOTAP (1,2-bis(oleoyloxy)-3-(trimethylammonio)propane) liposomes.

Similarly, anionic and neutral liposomes are readily available, such as
5 from Avanti Polar Lipids (Birmingham, AL), or can be easily prepared using readily available materials. Such materials include phosphatidyl choline, cholesterol, phosphatidyl ethanolamine, dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), dioleoylphosphatidyl ethanolamine (DOPE), among others. These materials can also be mixed with the DOTMA and DOTAP
10 starting materials in appropriate ratios. Methods for making liposomes using these materials are well known in the art.

The liposomes can comprise multilammellar vesicles (MLVs), small unilamellar vesicles (SUVs), or large unilamellar vesicles (LUVs). The various liposome-nucleic acid complexes are prepared using methods known in the art. *See*,
15 e.g., Straubinger *et al.*, *METHODS OF IMMUNOLOGY* (1983), Vol. 101, pp. 512-527; Szoka *et al.*, *Proc. Nat'l Acad. Sci. USA* 87:3410-3414, 1990; Papahadjopoulos *et al.*, *Biochim. Biophys. Acta* 394:483, 1975; Wilson *et al.*, *Cell* 17:77, 1979; Deamer and Bangham, *Biochim. Biophys. Acta* 443:629, 1976; Ostro *et al.*, *Biochem. Biophys. Res. Commun.* 76:836, 1977; Fraley *et al.*, *Proc. Nat'l Acad. Sci. USA* 76:3348, 1979; Enoch
20 and Strittmatter, *Proc. Nat'l Acad. Sci. USA* 76:145, 1979; Fraley *et al.*, *J. Biol. Chem.* 255:10431, 1980; Szoka and Papahadjopoulos, *Proc. Nat'l Acad. Sci. USA* 75:145, 1979; and Schaefer-Ridder *et al.*, *Science* 215:166, 1982.

In addition, lipoproteins can be included with a metastatic marker subgenomic polynucleotide for delivery to a cell. Examples of such lipoproteins
25 include chylomicrons, HDL, IDL, LDL, and VLDL. Mutants, fragments, or fusions of these proteins can also be used. Modifications of naturally occurring lipoproteins can also be used, such as acetylated LDL. These lipoproteins can target the delivery of polynucleotides to cells expressing lipoprotein receptors. Preferably, if lipoproteins are included with a polynucleotide, no other targeting ligand is included in the composition.

In another embodiment, naked metastatic marker subgenomic polynucleotide molecules are used as gene delivery vehicles, as described in WO 90/11092 and U.S. Patent 5,580,859. Such gene delivery vehicles can be either metastatic marker DNA or RNA and, in certain embodiments, are linked to killed
5 adenovirus. Curiel *et al.*, *Hum. Gene Ther.* 3:147-154, 1992. Other suitable vehicles include DNA-ligand (Wu *et al.*, *J. Biol. Chem.* 264:16985-16987, 1989), lipid-DNA combinations (Felgner *et al.*, *Proc. Nat'l Acad. Sci. USA* 84:7413-7417, 1989), liposomes (Wang *et al.*, *Proc. Nat'l Acad. Sci.* 84:7851-7855, 1987) and microprojectiles (Williams *et al.*, *Proc. Nat'l Acad. Sci.* 88:2726-2730, 1991).

10 One can increase the efficiency of naked metastatic marker subgenomic polynucleotide uptake into cells by coating the polynucleotides onto biodegradable latex beads. This approach takes advantage of the observation that latex beads, when incubated with cells in culture, are efficiently transported and concentrated in the perinuclear region of the cells. The beads will then be transported into cells when
15 injected into muscle. Metastatic marker subgenomic polynucleotide-coated latex beads will be efficiently transported into cells after endocytosis is initiated by the latex beads and thus increase gene transfer and expression efficiency. This method can be improved further by treating the beads to increase their hydrophobicity, thereby facilitating the disruption of the endosome and release of metastatic marker
20 subgenomic polynucleotides into the cytoplasm.

The invention provides a method of detecting metastatic marker gene expression in a biological sample. Detection of metastatic marker gene expression is useful, for example, for identifying metastases or for determining metastatic potential in a tissue sample, preferably a tumor. Appropriate treatment regimens can then be
25 designed for patients who are at risk for developing metastatic cancers in other organs of the body.

The body sample can be, for example, a solid tissue or a fluid sample. Protein or nucleic acid expression products can be detected in the body sample. In one embodiment, the body sample is assayed for the presence of a metastatic marker
30 protein. A metastatic marker protein comprises a sequence encoded by a nucleotide

sequence shown in SEQ ID NOS:1-85 or its complement and can be detected using the marker protein-specific antibodies of the present invention. The antibodies can be labeled, for example, with a radioactive, fluorescent, biotinylated, or enzymatic tag and detected directly, or can be detected using indirect immunochemical methods, using a
5 labeled secondary antibody. The presence of the metastatic marker proteins can be assayed, for example, in tissue sections by immunocytochemistry, or in lysates, using Western blotting, as is known in the art.

In another embodiment, the body sample is assayed for the presence of marker protein mRNA. A sample can be contacted with a nucleic acid hybridization
10 probe capable of hybridizing with the mRNA corresponding the selected polypeptide. Still further, the sample can be subjected to a Northern blotting technique to detect mRNA, indicating expression of the polypeptide. For those techniques in which mRNA is detected, the sample can be subjected to a nucleic acid amplification process whereby the mRNA molecule or a selected part thereof is amplified using appropriate nucleotide
15 primers. Other RNA detection techniques can also be used, including, but not limited to, *in situ* hybridization.

Marker protein-specific probes can be generated using the cDNA sequences disclosed in SEQ ID NOS:1-85. The probes are preferably at least 15 to 50 nucleotides in length, although they can be at least 8, 10, 11, 12, 20, 25, 30, 35, 40, 45,
20 60, 75, or 100 or more nucleotides in length. The probes can be synthesized chemically or can be generated from longer polynucleotides using restriction enzymes. The probes can be labeled, for example, with a radioactive, biotinylated, or fluorescent tag.

Optionally, the level of a particular metastatic marker expression product in a body sample can be quantitated. Quantitation can be accomplished, for example,
25 by comparing the level of expression product detected in the body sample with the amounts of product present in a standard curve. A comparison can be made visually or using a technique such as densitometry, with or without computerized assistance. For use as controls, body samples can be isolated from other humans, other non-cancerous organs of the patient being tested, or non-metastatic breast or colon cancer from the
30 patient being tested.

Polynucleotides encoding metastatic marker-specific reagents of the invention, such as antibodies and nucleotide probes, can be supplied in a kit for detecting marker gene expression products in a biological sample. The kit can also contain buffers or labeling components, as well as instructions for using the reagents to
5 detect the marker expression products in the biological sample.

If expression of a metastatic marker gene having a nucleotide sequence shown in SEQ ID NOS:2, 4, 9, 13, 14, 19, 26, 29, 39-41, 48, 55, 57, 60, 63, 64, 72, 73, 82, or 83 is detected, the biological sample contains cancer cells which will likely metastasize to the lung. If expression of a metastatic marker gene having a nucleotide
10 sequence shown in SEQ ID NOS:1, 5, 11, 18, 20, 22, 24, 30, 33, 35, 36, 38, 45, 52, 58, 65, 66, 70, 74, 76, or 80 is detected, the biological sample contains cancer cells which will likely metastasize to the bone and/or lung. On the other hand, if expression of a metastatic marker gene having a nucleotide sequence shown in SEQ ID NOS:3, 7, 8, 10, 12, 15-17, 21, 23, 25, 28, 31, 34, 37, 42-44, 46, 47, 49-51, 53, 59, 61, 62, 67, 68, 75, 77-
15 79, 81, 84, or 85 is detected, the biological sample contains cancer cells which will likely not metastasize. Detection of expression of a metastatic marker gene comprising the nucleotide sequence shown in SEQ ID NO:56 also indicates that the biological sample contains cancer cells which will likely metastasize. This information can be used, for example, to design treatment regimens. Treatment regimens can include
20 altering expression of one or more metastatic marker genes, as desired. Metastatic marker gene expression can be altered for therapeutic purposes, as described below, or can be used to identify therapeutic agents.

In one embodiment of the invention, expression of a metastatic marker gene whose expression is up-regulated in metastatic cancer is decreased using a
25 ribozyme, an RNA molecule with catalytic activity. *See, e.g.,* Cech, 1987, *Science* 236: 1532-1539; Cech, 1990, *Ann. Rev. Biochem.* 59:543-568; Cech, 1992, *Curr. Opin. Struct. Biol.* 2: 605-609; Couture and Stinchcomb, 1996, *Trends Genet.* 12: 510-515. Ribozymes can be used to inhibit gene function by cleaving an RNA sequence, as is known in the art (*e.g.,* Haseloff *et al.*, U.S. 5,641,673).

Coding sequences of metastatic marker genes can be used to generate ribozymes which will specifically bind to mRNA transcribed from a metastatic marker gene. Methods of designing and constructing ribozymes which can cleave other RNA molecules in trans in a highly sequence specific manner have been developed and
5 described in the art (see Haseloff, J. *et al.* (1988), *Nature* 334:585-591). For example, the cleavage activity of ribozymes can be targeted to specific RNAs by engineering a discrete "hybridization" region into the ribozyme. The hybridization region contains a sequence complementary to the target RNA and thus specifically hybridizes with the target (see, for example, Gerlach, W. L. *et al.*, EP 321,201). Longer complementary
10 sequences can be used to increase the affinity of the hybridization sequence for the target. The hybridizing and cleavage regions of the ribozyme can be integrally related; thus, upon hybridizing to the target RNA through the complementary regions, the catalytic region of the ribozyme can cleave the target.

Ribozymes can be introduced into cells as part of a DNA construct, as is
15 known in the art. The DNA construct can also include transcriptional regulatory elements, such as a promoter element, an enhancer or UAS element, and a transcriptional terminator signal, for controlling the transcription of the ribozyme in the cells.

Mechanical methods, such as microinjection, liposome-mediated
20 transfection, electroporation, or calcium phosphate precipitation, can be used to introduce a ribozyme-containing DNA construct into cells whose division it is desired to decrease, as described above. Alternatively, if it is desired that a DNA construct be stably retained by the cells, the DNA construct can be supplied on a plasmid and maintained as a separate element or integrated into the genome of the cells, as is known
25 in the art.

As taught in Haseloff *et al.*, U.S. 5,641,673, ribozymes can be engineered so that their expression will occur in response to factors which induce expression of metastatic marker genes. Ribozymes can also be engineered to provide an additional level of regulation, so that destruction of mRNA occurs only when both a
30 ribozyme and a metastatic marker gene are expressed in the cells.

Expression of a metastatic marker gene can also be altered using an antisense oligonucleotide sequence. The antisense sequence is complementary to at least a portion of the coding sequence of a metastatic marker gene having a nucleotide sequence shown in SEQ ID NOS: 1-85. The complement of a nucleotide sequence shown in SEQ ID NOS: 1-85 is a contiguous sequence of nucleotides which form Watson-Crick basepairs with a contiguous nucleotide sequence shown in SEQ ID NOS: 1-85.

Preferably, the antisense oligonucleotide sequence is at least six nucleotides in length, but can be at least about 8, 12, 15, 20, 25, 30, 35, 40, 45, or 50 nucleotides long. Longer sequences can also be used. Antisense oligonucleotide molecules can be provided in a DNA construct and introduced into cells whose division is to be decreased, as described above.

Antisense oligonucleotides can comprise deoxyribonucleotides, ribonucleotides, or a combination of both. Oligonucleotides can be synthesized manually or by an automated synthesizer, by covalently linking the 5' end of one nucleotide with the 3' end of another nucleotide with non-phosphodiester internucleotide linkages such as alkylphosphonates, phosphorothioates, phosphorodithioates, alkylphosphonothioates, alkylphosphonates, phosphoramidates, phosphate esters, carbamates, acetamides, carboxymethyl esters, carbonates, and phosphate triesters. See Brown, 1994, *Meth. Mol. Biol.* 20:1-8; Sonveaux, 1994, *Meth. Mol. Biol.* 26:1-72; Uhlmann *et al.*, 1990, *Chem. Rev.* 90:543-583.

Although precise complementarity is not required for successful duplex formation between an antisense molecule and the complementary coding sequence of a metastatic marker gene, antisense molecules with no more than one mismatch are preferred. One skilled in the art can easily use the calculated melting point of a metastatic marker gene antisense-sense pair to determine the degree of mismatching which will be tolerated between a particular antisense oligonucleotide and a particular coding sequence of the selected gene.

Antisense oligonucleotides can be modified without affecting their ability to hybridize to a metastatic marker protein coding sequence. These

modifications can be internal or at one or both ends of the antisense molecule. For example, internucleoside phosphate linkages can be modified by adding cholesteryl or diamine moieties with varying numbers of carbon residues between the amino groups and terminal ribose. Modified bases and/or sugars, such as arabinose instead of ribose, or a 3', 5'-substituted oligonucleotide in which the 3' hydroxyl group or the 5' phosphate group are substituted, can also be employed in a modified antisense oligonucleotide. These modified oligonucleotides can be prepared by methods well known in the art. Agrawal et al., 1992, Trends Biotechnol. 10:152-158; Uhlmann *et al.*, 1990, *Chem. Rev.* 90:543-584; Uhlmann *et al.*, 1987, *Tetrahedron. Lett.* 215:3539-3542.

10 Antibodies of the invention which specifically bind to a metastatic marker protein can also be used to alter metastatic marker gene expression. By antibodies is meant antibodies and parts or derivatives thereof, such as single chain antibodies, that retain specific binding for the protein. Specific antibodies bind to metastatic marker proteins and prevent the proteins from functioning in the cell.

15 Polynucleotides encoding specific antibodies of the invention can be introduced into cells, as described above.

 Marker proteins of the present invention can be used to screen for drugs which have a therapeutic anti-metastatic effect. The effect of a test compound on metastatic marker protein synthesis can also be used to identify test compounds which

20 modulate metastasis. Test compounds which can be screened include any substances, whether natural products or synthetic, which can be administered to the subject. Libraries or mixtures of compounds can be tested. The compounds or substances can be those for which a pharmaceutical effect is previously known or unknown.

 A cell is contacted with a test compound. The cell can be any cell, such

25 as a colon cancer cell, which ordinarily synthesizes the metastatic marker protein being measured. For example, Tables 1 and 2 provide appropriate cell types which can be used for screening assays.

 Synthesis of metastatic marker proteins can be measured by any means for measuring protein synthesis known in the art, such as incorporation of labeled amino

30 acids into proteins and detection of labeled metastatic marker proteins in a

polyacrylamide gel. The amount of metastatic marker proteins can be detected, for example, using metastatic marker protein-specific antibodies of the invention in Western blots. The amount of the metastatic marker proteins synthesized in the presence or absence of a test compound can be determined by any means known in the art, such as comparison of the amount of metastatic marker protein synthesized with the amount of the metastatic marker proteins present in a standard curve.

The effect of a test compound on metastatic marker protein synthesis can also be measured by Northern blot analysis, by measuring the amount of metastatic marker protein mRNA expression in response to the test compound using metastatic marker protein specific nucleotide probes of the invention, as is known in the art.

Typically, biological sample is contacted with a range of concentrations of the test compound, such as 1.0 nM, 5.0 nM, 10 nM, 50 nM, 100 nM, 500 nM, 1 mM, 10 mM, 50 mM, and 100 mM. Preferably, the test compound increases or decreases expression of a metastatic marker protein by 60%, 75%, or 80%. More preferably, an increase or decrease of 85%, 90%, 95%, or 98% is achieved.

The invention provides compositions for increasing or decreasing expression of metastatic marker protein. Therapeutic compositions for increasing metastatic marker gene expression are desirable for markers which are down-regulated in metastatic cells. These compositions comprise polynucleotides encoding all or at least a portion of a metastatic marker protein gene expression product. Preferably, the therapeutic composition contains an expression construct comprising a promoter and a polynucleotide segment encoding at least a portion of the metastatic marker protein which is effective to increase or decrease metastatic potential. Portions of metastatic marker genes or proteins which are effective to decrease metastatic potential of a cell can be determined, for example, by introducing various portions of metastatic marker genes or polypeptides into metastatic cell lines, such as MDA-MB-231, MDA-MB-435, Km12C, or Km12L4, and assaying the division rate of the cells or the ability of the cells to form metastases when implanted *in vivo*, as is known in the art. Non-metastatic cell lines, such as MCF-7, can be used to assay the ability of a portion of a metastatic marker protein to increase expression of a metastatic marker gene.

Within the expression construct, the polynucleotide segment is located downstream from the promoter, and transcription of the polynucleotide segment initiates at the promoter. A more complete description of gene transfer vectors, especially retroviral vectors is contained in U.S. Serial No. 08/869,309, which is
5 incorporated herein by reference.

Decreased metastatic marker gene expression is desired in conditions in which the marker gene is up-regulated in metastatic cancer. Therapeutic compositions for treating these disorders comprise a polynucleotide encoding a reagent which specifically binds to a metastatic marker protein expression product, as disclosed herein.

10 Metastatic marker therapeutic compositions of the invention can comprise a pharmaceutically acceptable carrier. Pharmaceutically acceptable carriers are well known to those in the art. Such carriers include, but are not limited to, large, slowly metabolized macromolecules, such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus
15 particles. Pharmaceutically acceptable salts can also be used in the composition, for example, mineral salts such as hydrochlorides, hydrobromides, phosphates, or sulfates, as well as the salts of organic acids such as acetates, propionates, malonates, or benzoates.

Therapeutic compositions can also contain liquids, such as water, saline,
20 glycerol, and ethanol, as well as substances such as wetting agents, emulsifying agents, or pH buffering agents. Liposomes, such as those described in U.S. 5,422,120, WO 95/13796, WO 91/14445, or EP 524,968 B1, can also be used as a carrier for the therapeutic composition.

Typically, a therapeutic metastatic marker composition is prepared as an
25 injectable, either as a liquid solution or suspension; however, solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection can also be prepared. A metastatic marker composition can also be formulated into an enteric coated tablet or gel capsule according to known methods in the art, such as those described in U.S. 4,853,230, EP 225,189, AU 9,224,296, and AU 9,230,801.

Administration of the metastatic marker therapeutic agents of the invention can include local or systemic administration, including injection, oral administration, particle gun, or catheterized administration, and topical administration. Various methods can be used to administer a therapeutic metastatic marker composition
5 directly to a specific site in the body.

For treatment of tumors, including metastatic lesions, for example, a therapeutic metastatic marker composition can be injected several times in several different locations within the body of tumor. Alternatively, arteries which serve a tumor can be identified, and a therapeutic composition injected into such an artery, in
10 order to deliver the composition directly into the tumor.

A tumor which has a necrotic center can be aspirated and the composition injected directly into the now empty center of the tumor. A therapeutic metastatic marker composition can be directly administered to the surface of a tumor, for example, by topical application of the composition. X-ray imaging can be used to
15 assist in certain of the above delivery methods. Combination therapeutic agents, including a metastatic marker proteins or polypeptide or a metastatic marker subgenomic polynucleotide and other therapeutic agents, can be administered simultaneously or sequentially.

Receptor-mediated targeted delivery can be used to deliver therapeutic
20 compositions containing metastatic marker subgenomic polynucleotides, proteins, or reagents such as antibodies, ribozymes, or antisense oligonucleotides to specific tissues. Receptor-mediated delivery techniques are described in, for example, Findeis et al. (1993), *Trends in Biotechnol.* 11, 202-05; Chiou et al. (1994), *GENE THERAPEUTICS: METHODS AND APPLICATIONS OF DIRECT GENE TRANSFER* (J.A. Wolff, ed.); Wu & Wu
25 (1988), *J. Biol. Chem.* 263, 621-24; Wu et al. (1994), *J. Biol. Chem.* 269, 542-46; Zenke et al. (1990), *Proc. Nat'l Acad. Sci. U.S.A.* 87, 3655-59; Wu et al. (1991), *J. Biol. Chem.* 266, 338-42.

Alternatively, a metastatic marker therapeutic composition can be introduced into human cells *ex vivo*, and the cells then replaced into the human. Cells
30 can be removed from a variety of locations including, for example, from a selected

tumor or from an affected organ. In addition, a therapeutic composition can be inserted into non-affected, for example, dermal fibroblasts or peripheral blood leukocytes. If desired, particular fractions of cells such as a T cell subset or stem cells can also be specifically removed from the blood (*see*, for example, PCT WO 91/16116). The removed cells can then be contacted with a metastatic marker therapeutic composition utilizing any of the above-described techniques, followed by the return of the cells to the human, preferably to or within the vicinity of a tumor or other site to be treated. The methods described above can additionally comprise the steps of depleting fibroblasts or other non-contaminating tumor cells subsequent to removing tumor cells from a human, and/or the step of inactivating the cells, for example, by irradiation.

Both the dose of a metastatic marker composition and the means of administration can be determined based on the specific qualities of the therapeutic composition, the condition, age, and weight of the patient, the progression of the disease, and other relevant factors. Preferably, a therapeutic composition of the invention increases or decreases expression of the metastatic marker genes by 50%, 60%, 70%, or 80%. Most preferably, expression of the metastatic marker genes is increased or decreased by 90%, 95%, 99%, or 100%. The effectiveness of the mechanism chosen to alter expression of the metastatic marker genes can be assessed using methods well known in the art, such as hybridization of nucleotide probes to mRNA of the metastatic marker genes, quantitative RT-PCR, or detection of an the metastatic marker proteins using specific antibodies of the invention.

If the composition contains the metastatic marker proteins, polypeptide, or antibody, effective dosages of the composition are in the range of about 5 μ g to about 50 μ g/kg of patient body weight, about 50 μ g to about 5 mg/kg, about 100 μ g to about 500 μ g/kg of patient body weight, and about 200 to about 250 μ g/kg.

Therapeutic compositions containing metastatic marker subgenomic polynucleotides can be administered in a range of about 100 ng to about 200 mg of DNA for local administration. Concentration ranges of about 500 ng to about 50 mg, about 1 μ g to about 2 mg, about 5 μ g to about 500 μ g, and about 20 μ g to about 100 μ g of DNA can also be used during a gene therapy protocol. Factors such as method of

action and efficacy of transformation and expression are considerations that will affect the dosage required for ultimate efficacy of the metastatic marker subgenomic polynucleotides. Where greater expression is desired over a larger area of tissue, larger amounts of metastatic marker subgenomic polynucleotides or the same amounts
5 readministered in a successive protocol of administrations, or several administrations to different adjacent or close tissue portions of, for example, a tumor site, can be required to effect a positive therapeutic outcome. In all cases, routine experimentation in clinical trials will determine specific ranges for optimal therapeutic effect.

Expression of an endogenous metastatic marker gene in a cell can also be
10 altered by introducing in frame with the endogenous metastatic marker gene a DNA construct comprising a metastatic marker protein targeting sequence, a regulatory sequence, an exon, and an unpaired splice donor site by homologous recombination, such that a homologously recombinant cell comprising the DNA construct is formed. The new transcription unit can be used to turn the metastatic marker gene on or off as
15 desired. This method of affecting endogenous gene expression is taught in U.S. Patent No. 5,641,670, which is incorporated herein by reference.

The targeting sequence is a segment of at least 10, 12, 15, 20, or 50 contiguous nucleotides selected from the nucleotide sequences shown in SEQ ID NOS:1-85 or the complements thereof. The transcription unit is located upstream of a
20 coding sequence of the endogenous metastatic marker protein gene. The exogenous regulatory sequence directs transcription of the coding sequence of the metastatic marker genes.

A metastatic marker subgenomic polynucleotide can also be delivered to subjects for the purpose of screening test compounds for those which are useful for
25 enhancing transfer of metastatic marker subgenomic polynucleotides to the cell or for enhancing subsequent biological effects of metastatic marker subgenomic polynucleotides within the cell. Such biological effects include hybridization to complementary metastatic marker mRNA and inhibition of its translation, expression of a metastatic marker subgenomic polynucleotide to form metastatic marker mRNA
30 and/or metastatic marker protein, and replication and integration of a metastatic marker

subgenomic polynucleotide. The subject can be a cell culture or an animal, preferably a mammal, more preferably a human.

Test compounds which can be screened include any substances, whether natural products or synthetic, which can be administered to the subject. Libraries or mixtures of compounds can be tested. The compounds or substances can be those for which a pharmaceutical effect is previously known or unknown. The compounds or substances can be delivered before, after, or concomitantly with a metastatic marker subgenomic polynucleotide. They can be administered separately or in admixture with a metastatic marker subgenomic polynucleotide.

Integration of a delivered metastatic marker subgenomic polynucleotide can be monitored by any means known in the art. For example, Southern blotting of the delivered metastatic marker subgenomic polynucleotide can be performed. A change in the size of the fragments of a delivered polynucleotide indicates integration. Replication of a delivered polynucleotide can be monitored *inter alia* by detecting incorporation of labeled nucleotides combined with hybridization to a metastatic marker probe. Expression of metastatic marker subgenomic polynucleotide can be monitored by detecting production of metastatic marker mRNA which hybridizes to the delivered polynucleotide or by detecting metastatic marker protein. Metastatic marker protein can be detected immunologically. Thus, the delivery of metastatic marker subgenomic polynucleotides according to the present invention provides an excellent system for screening test compounds for their ability to enhance transfer of metastatic marker subgenomic polynucleotides to a cell, by enhancing delivery, integration, hybridization, expression, replication or integration in a cell *in vitro* or in an animal, preferably a mammal, more preferably a human.

The above disclosure generally describes the present invention. A more complete understanding can be obtained by reference to the following specific examples which are provided herein for purposes of illustration only, and are not intended to limit the scope of the invention.

EXAMPLE 1

DIFFERENTIALLY EXPRESSED GENES

This example demonstrates polynucleotides that are differentially
5 expressed in human breast or colon cancer cell lines.

Human cell lines used to identify differentially expressed polynucleotides are the human breast cancer cell lines MCF-7 (non-metastatic), MDA-MB-231 (metastatic to bone and/or lung), and MDA-MB-435 (metastatic to lung) (Brinkley and Cailleau, 1980, *Cancer Res.* 40:3118), and the colon cancer cell lines
10 Km12C (low metastatic) and Km12L4A (highly metastatic) (Morikawa *et al.*, 1988, *Cancer Res.* 48:1943-1948).

RNA was prepared from each cell line and reverse transcribed to form cDNA. The cDNA was amplified using random primers. Amplification products were visualized on a sequencing gel, and cDNA corresponding to mRNA which was
15 differentially expressed in the cell lines was identified.

Expression patterns and sequence identification numbers of novel metastatic marker polynucleotides are shown in Table 1.

Expression patterns and sequence identification numbers of metastatic marker polynucleotides which correspond to known genes are shown in Table 2, and the
20 corresponding proteins are described below.

Osteopontin (SEQ ID NO:64) (OPN or Sppl for secreted phosphoprotein 1) is a secreted extracellular matrix protein, often expressed during wound healing, involved in osteoclastic differentiation and activation, as described in Heymann *et al.*, 1998, *Cytokine* 10:155-168. Osteopontin is found in bone and other epithelial cells, and
25 has been shown to stimulate proliferation of a quiescent subpopulation of prostate epithelial cells (see Elgavish *et al.*, 1998, *Prostate* 35:83-94).

Osteopontin is implicated during the development of diabetic nephropathy (Fischer *et al.*, 1998, *Diabetes* 47:1512-1518); the process of cartilage-to-bone transition during rigid bone healing after bone fracture (Nakase *et al.*, 1998, *Acta*
30 *Histochem* 100:287-295); wound healing by an interaction with the receptor integrin

alpha(v)beta 3 after focal stroke (Ellison *et al.*, 1998, *Stroke* 29:1698-1706); integrin receptor binding and signaling during cell attachment and mechanical stimulation of osteoblasts (Carvalho *et al.*, 1998, *J. Cell Biochem* 70:376-390); kidney morphogenesis (Denda *et al.*, 1998, *Mol. Biol. Cell* 9:1425-1435); and as an interstitial chemoattractant in renal inflammation (Rovin and Phan, 1998, *Am. J. Kidney Dis.* 31:1065-1084). Mice lacking the osteopontin gene showed modulation in osteoclast differentiation from wild type mice (see Rittling *et al.*, 1998, *J. Bone Miner Res.* 13:1101-1111).

Osteopontin is synthesized by monocytes and macrophages within injury sites, and can promote leukocyte adhesion through the alpha 4beta1 integrin, as described in Bayless *et al.*, 1998, *J. Cell Sci.* 111:1165-1174. Osteopontin is transcriptionally regulated by retinoic acid (see Manji *et al.*, 1998, *J. Cell Physiol.* 176:1-9); preferentially expressed in high grade metastatic brain tumors compared to low grade brain tumors, and inducible by tissue plasminogen activator (tPA) in glioma cell lines (see Tucker *et al.*, 1998, *Anticancer Res.* 18:807-812). Osteopontin is expressed in about 73% of primary gastric carcinoma tissues and correlated with the progression of human gastric carcinoma and lymphogenous metastasis (see Ue *et al.*, 1998, *Int. J. Cancer* 79:127-132).

Nip (SEQ ID NO:65) is described in Boyd *et al.*, 1994, *Cell* 79:341-351. Adenovirus E1B 19 kDa protein protects against cell death induced by viral infection and external stimuli, and can be functionally substituted with the Bcl-2 protooncogene. E1B 19 kDa interacting proteins (Nip1, Nip2, and Nip3) were discovered in yeast two-hybrid studies conducted to discern proteins that interact with 19 kDa protein, as described by Boyd *et al.*, *supra*. Nip 1, 2, and 3 interact with discrete domains of E1B 19 kDa, and similarly also interact with Bcl-2, in both cases promoting cell survival.

Ca-dependent protease (SEQ ID NO:66) is Ca^{+2} -dependent protease (also called calpain), activity of which is present in every vertebrate cell that has been examined. Ca^{+2} -dependent protease activity is associated with cleavages that alter regulation of various enzyme activities, with remodeling or disassembly of the cell cytoskeleton, and with cleavages of hormone receptors (see Goll *et al.*, 1992, *Bioessays* 14(8):549-556). Ca^{+2} -dependent protease activity is regulated by binding of Ca^{+2} to

specific sites on the calpain molecule, with binding to each site generating a specific response correlated with a specific activity (e.g., proteolytic activity, calpastatin binding, etc.), as described in Goll *et al.* Excessive activation of the Ca^{2+} -dependent protease calpain may play a role in the pathology of disorders including cerebral ischemia, cataract, myocardial ischemia, muscular dystrophy, and platelet aggregation. Therapeutic applications include selective Ca^{2+} -dependent protease inhibition, as described in Wang and Yuen, 1994, *Trends Pharmacol. Sci.* 15(11):412-419.

IGF-R (insulin-like growth factor receptor) (SEQ ID NO:67) is a transmembrane tyrosine kinase linked to the ras-raf-MAPK(mitogen-activated protein kinase) cascade and required for the cell to progress through the cell cycle (Werner and Roith, 1997, *Crit. Rev. Oncog* 8(1):71-92). IGF-R mediates mitogenesis, growth hormone action, cell survival and transformation to and maintenance of the malignant phenotype. IGF-R is a member of the growth factor receptor tyrosine kinase superfamily, exists as covalent cross-linked dimers where each monomer is composed of two subunits, and is bound by ligand in the extracellular domain (McInnes and Sykes, 1997, *Biopolymers* 43(5):339-366).

The domains of the IGF-R are described in Sepp-Lorenzino, 1998, *Breast Cancer Res Treat* 47(3):235-253, including domains responsible for mitogenesis, transformation, and protection from apoptosis. IGF-R expression is increased in breast cancer cells derived from tumor tissue and cell lines, as described in Surmacz *et al.*, 1998, *Breast Cancer Res Treat* 47(3):255-267, and increased IGF-R may increase tumor mass and/or aid tumor recurrence by promoting proliferation, cell survival, and cell-cell interactions. Human pancreatic cancers overexpress IGF-R and its ligand (Korc, 1998, *Surg Oncol Clin N Am* 7(1): 25-41), and expression of IGF-I and IGF-R is determined to be a prognostic factor (reflecting the interaction between the neoplastic cells and their microenvironment) for lymphocytic infiltration in thyroid carcinomas (Fonseca *et al.*, 1997, *Verh Dtsch Ges Pathol* 81:82-96).

ILGF-BP5 (SEQ ID NO:68) is insulin-like growth factor binding protein 5, described in Allander *et al.*, 1994, *J. Biol. Chem.* 269:10891-10898. The gene and promoter for IGF-BP5 are characterized by Allander *et al.*, 1994, *J. Biol Chem.*

269:10891-10898, and some general actions of IGF-BPs are described in Chan and Spencer, 1997, *Endocrine* 7:95-97. Potential impact of IGF-BPs on cancer cell growth is described in Oh, 1997, *Endocrine* 7:111-113, and Oh, 1998, *Breast Cancer Res Treat* 47:283-293. IGF-BP5 is expressed during brain development: IGF-BP5 and IGF-I
5 mRNAs are synchronously coexpressed in principal neurons of sensory relay systems, including the olfactory bulb, medial and dorsal lateral geniculate bodies, and ventral tier, cochlear, lemniscal, and vestibular nuclei, and are transiently coexpressed in principal neurons of the anterodorsal nucleus, as described in Bondy and Lee, 1993, *J. Neurosci* 13(12):5092-5104. IGF-BP5 is expressed by luminal or cumulus granulosa
10 cells in virtually all follicles, and is highly abundant in stromal interstitial cells of the mature ovary (see Zhou and Bondy, 1993, *Biol. Reprod* 48:467-482). IGF-BP5 induction is strongly stimulated during differentiation of skeletal myoblasts and is correlated with IGF-R activation as described in Rousse *et al.*, 1998, *Endocrinology* 139:1487-1493. IGF-BP5 and other components of the IGF system are critical in
15 postnatal brain development (see Lee *et al.*, 1996, *J. Cereb Blood Flow Metab* 16:227-236).

IGF-BP5 stimulates bone cell proliferation by an IGF-independent mechanism involving IGF-BP5-specific cell surface binding sites, as described in Mohan *et al.*, 1995, *J. Biol Chem* 270:20424-20431. In connective tissue cell types,
20 IGF-BP5 has a lowered binding affinity to the extracellular matrix which allows IGF-I to better equilibrate with the receptors which in turn potentiates IGF-I action on fibroblasts and smooth muscle cells (Clemmons, *Mol Cell Endocrinology* 140:19-24).

Lactate dehydrogenase (SEQ ID NO:69) is a member of the LDH group of tetrameric enzymes with five isoforms composed of combinations of two subunits,
25 LDH-A and LDH-B. Shim *et al.*, 1997, *Proc. Nat'l Acad. Sci.* 94:6658-6663, described the relationship between LDH-A and neoplasia. In particular, overexpression on LDH-A may contribute to altered metabolism that confers neoplastic growth advantage. The expression pattern of LDH in the present invention is consistent, in that LDH expression is higher in two metastatic breast cancer cell lines than in a non-metastatic
30 breast cancer cell line (Table 2). High or increasing lactate dehydrogenase (LDH) levels

in tumor tissue and cells is associated with poor survival rate in small cell lung carcinoma (SCLC), as described in Ray *et al.*, 1998, *Cancer Detect Prev* 22:293-304, making it a useful prognostic indicator for SCLC as discussed in Stokkel *et al.*, 1998, *J. Cancer Res Clin Oncol* 124:215-219.

5 Ufo TKR (SEQ ID NO:70) is described in Schulz *et al.*, 1993, *Oncogene* 8:509-513. This protein has been reported as a marker in tumors, but has not previously been reported in breast cancer. According to the present invention, expression is found in the MDA-MB-231 breast cancer cell line, but not in the MSF-7 or MDA-MB-435 cell lines. This gene and protein provide new markers for distinguishing breast cancer
10 tissue of different types of metastatic potential.

Initially isolated from primary human myeloid leukemia cells, the ufo oncogene (also called Axl or Ark) is a receptor tyrosine kinase (RTK). Its genomic structure is described in Schulz *et al.*, *supra.*, and its differential expression is described in Challier *et al.*, 1996, *Leukemia* 10:781-787. The ufo protein is a member of a class
15 of RTKs having two fibronectin type III domains and two immunoglobulin-like domains present in the extracellular portion, and is preferentially expressed in monocytes, stromal cells, and some CD34-positive progenitor cells (Neubauer *et al.*, 1997, *Leuk Lymphoma* 25:91-96). Ufo has an extracellular structure similar to neural cell adhesion molecules, and has direct or indirect binding sites for PLCgamma, GRB2,
20 c-src, and lck (Braunger *et al.*, 1997, *Oncogene* 14:2619-2631).

eIF-2 (SEQ ID NO:71) is a translation initiation factor, and functions as a heterotrimeric GTP-binding protein involved in the recruitment of methionyl-tRNA to the 40 S ribosomal subunit (Gasper *et al.*, 1994, *J. Biol. Chem.* 269:3415-3422). According to the present invention, higher expression is found in two metastatic breast
25 cancer cell lines and not in cell line MCF-7.

eIF-2 is involved in introducing the initiator tRNA into the translation mechanism and performing the first step in the peptide chain elongation cycle. eIF-2 is associated with a 5 subunit molecule having GTP recycling function called eIF-2B (Kyrpides and Woese, 1998, *Proc. Nat'l Acad. Sci. USA* 95:3726-3730, and Kimball *et al.*, 1998, *J. Biol. Chem.* 273:12841-12845).
30

eIF-2 has subunits alpha and beta. eIF-2alpha is phosphorylated at Ser 51 and then modulates the interaction of eIF-2 and eIF-2B, as described in Kimball *et al.*, 1998, *Protein Expr. Purif.* 12:415-419, Kimball *et al.*, 1998, *J. Biol. Chem.* 273:3039-3044, and Pavitt 1998, *Genes Dev.* 12:514-526. It is reported that by
5 regulating translation initiation, control of cell growth and division in eukaryotic cells is achieved: for example, clotrimazole, a potent anti-proliferative agent *in vitro* and *in vivo*, depletes intracellular Ca^{+2} stores, which activates PKR, resulting in the phosphorylation of eIF-2alpha, and the ultimate inhibition of protein synthesis and blockage of the cell cycle in G1 phase (Aktas *et al.*, 1998, *Proc. Nat'l Acad. Sci. USA*
10 95:8280-8285). Additionally, Kim *et al.*, 1998, *Mol. Med.* 4:179-190, show that nitric oxide (NO) suppresses protein synthesis in cell types including human ovarian tumor cells by stimulating phosphorylation of eIF-2alpha.

Glutaminyl cyclase (SEQ ID NO:72) is described by Song *et al.*, 1994, *J. Mol. Endocrinol.* 13:77-86, and is expressed most highly in the most metastatic cell
15 line MDA-MB-435, as compared to less metastatic line MDA-MB-231 and non-metastatic line MCF-7. Glutaminyl cyclase (also called glutamine cyclotransferase) converts glutaminyl-peptides (such as gonadotropin-releasing hormone and thyrotropin-releasing hormone) into pyroglutaminyl-peptides, as described in Busby *et al.*, 1987, *J. Biol. Chem.* 262:8532-8536, Fischer and Spiess, 1987, *Proc. Nat'l Acad. Sci. USA*
20 84:3628-3632, and Pohl *et al.*, 1991, *Proc. Nat'l Acad. Sci.* 88:10059-10063. Cloning and sequence analysis of glutaminyl cyclase derived from a human pituitary cDNA library is described in Song *et al.*, 1994, *J. Mol. Endocrinol.* 13:77-86. Studies on the catalytic pathway of glutaminyl cyclase and its substrate specificity are described in Gololobov *et al.*, 1996, *Biol. Chem. Hoppe Seyler* 377:395-398. Assays for the
25 presence of glutaminyl cyclase activity are described in Koger *et al.*, 1989, *Method Enzymol.* 168:358-365 and Houseknecht *et al.*, 1998, *Biotechniques* 24:346.

gp130 (SEQ ID NO:73) is transmembrane protein glycoprotein 130. gp130 is a signal transducing shared component of the receptor complexes for the interleukin-6 (IL-6)-type cytokines (Hirano *et al.*, 1997, *Cytokine Growth Factor Rev.*
30 8:241-252), including IL-6, IL-11, leukemia inhibitor factor (LIF), oncostatin M

(OSM), ciliary neurotrophic factor and cardiotrophin-1. The N-terminal of gp130 is an extracellular immunoglobulin-like portion of the protein (Hammacher *et al.*, 1998, *J. Biol. Chem.* 273:22701-22707). Signal transduction including gp130 occurs through the gp130/Jak/STAT pathway 1 (Heinrich 1998, *Biochem. J.* 334:297-314). The
5 cytokines acting through the pathway that includes gp130 (also called gp130 cytokines) exhibit pleiotropic biological activities including immune, hematopoietic, and neural effects (Nakashima and Taga, 1998, *Semin Hematol.* 35:210-221, Thompson *et al.*, 1998, *Neuroscience* 84:1247-1255, Hirano, 1998, *Int. Rev. Immunol.* 16:249-284, Marz *et al.*, 1997, *Eur. J. Neurosci.* 9:2765-2773, and Betz and Muller, 1998, *Int Immunol*
10 10:1175-1184).

gp130 cytokines are reported to control survival and proliferation of myeloma cell lines and primary myeloma cells (Klein, 1998, *Curr. Opin. Hematol.* 5:186-191). gp130 is expressed in the majority of renal cell carcinomas and has an important role in the proliferation of some renal cell carcinoma cell lines (Costes *et al.*,
15 1997, *J. Clin. Pathol.* 50:835-840).

E-cadherin (SEQ ID NO:75) is a member of a family of glycoproteins responsible for calcium-dependent cell-cell adhesion and is implicated in maintaining cytoskeletal integrity. Epithelial cadherin (E-cadherin) mediated cell adhesion system in cancer cells is inactivated by multiple mechanisms corresponding to the pathological
20 features of the particular tumor type (Hirohashi, 1998, *Am J Pathol* 153:333-339). In general the cadherin system mediates Ca^{2+} -dependent homophilic cell-cell adhesion. Transcriptional inactivation of E-cadherin expression occurs frequently in tumor progression, and thus inactivation or downregulation of E-cadherin plays a significant role in multistage carcinogenesis (Hirohashi, 1998, *Am J Pathol* 153:333-339).

25 E-cadherin is characterized as a tumor suppressor of the metastatic phenotype, as described in MacGrogan and Bookstein, 1997, *Semin Cancer Biol* 8:11-19, and cadherins are important determinants of tissue morphology including invasive carcinoma as described in van der Linden, 1996, *Early Pregnancy* 2:5-14, and Yap, 1998, *Cancer Invest.* 16:252-261.

Mechanisms of action of cadherins are discussed in Daniel and Reynolds, 1997, *Bioessays* 19:883-891. The structure and function of cell adhesion molecules including E-cadherin are described in Joseph-Silverstein and Silverstein, 1998, *Cancer Invest.* 16:176-182, Yap *et al.*, 1997, *Annu. Rev. Cell Dev. Biol.* 13:119-146, and Uemura, 1998, *Cell* 93:1095-1098. Cell adhesion molecules including E-cadherin are potential targets for anti-cancer drugs and therapeutics to treat acute or chronic inflammatory disease as described in Buckley and Simmons, 1997, *Mol Med Today* 3:449-456, Moll and Moll, 1998, *Virchows Arch* 432:487-504.

According to the present invention, E-cadherin is expressed in non-metastatic breast cancer cell line MCF-7, and not in MDA-MB-231 and MDA-MB-435. The expression products are diagnostic markers indicating the metastatic potential of breast cancer tissue samples.

Serpin (SEQ ID NO:76), serine protease inhibitors, are a family of protease inhibitors that inhibit chymotrypsin-like serine proteases (Whisstock *et al.*, 1998, *Trends Biochem. Sci.* 23:63-67) and that have the unique ability to regulate their activity by changing the conformation of their reactive-center loop; studies of serpin variants provide definition for the functional domains of serpins that control the folding and link serpins mutations to disease (see Stein and Carrell, 1995, *Nat. Struct. Biol.* 2:96-113). Serine protease cleavage of proteins is essential to a wide variety of biological processes, and the cleavage is primarily regulated by the cleavage inhibitors, as described in Wright, 1996, *Bioessays* 18:453-464. Members of the serpin family include alpha 1-antitrypsin (AAT) (Carrell *et al.*, 1996, *Chest* 110:243S-247S), alpha2-anti-plasmin (PAI-1 and PAI-2) (Andreasen *et al.*, 1997, *Int. J. Cancer* 72:1-22), thrombin, urokinase plasminogen activator, and kallikrein (Turgeon and Houenou, 1997, *Brain Res Brain Res Rev* 25:85-95). Some serpins also have other activities including neuronal differentiating and survival activities (Becerra, 1997, *Adv. Exp. Med. Biol.* 425:332-237) and tumor suppression (Sager *et al.*, 1997, *Adv. Exp. Med. Biol.* 425:77-88). PAI-1 and PAI-2 are linked to cancer metastasis, as described in Andreasen *et al.*, 1997, *Int. J. Cancer* 72:1-22.

pS2 (SEQ ID NO:77) was isolated from MCF7 human breast cancer cells, as described in Takahashi *et al.*, 1990, *FEBS Letters* 261:283-286. pS2 is estrogen-regulated. Speiser *et al.*, 1997, *Anticancer Research* 17:679-684, reported that the pS2 status declined from well to poorly differentiated ovarian cancer. pS2 expression also is associated with a good prognosis in breast cancer patients. According to the present invention, pS2 is expressed in MCF-7 cells, but not in two metastatic breast cancer cell lines

pS2 (presenilin-2 or trefoil factor 1 (TFF 1)) is a trefoil polypeptide normally expressed in the mucosa of the gastrointestinal tract, and found ectopically in gastrointestinal inflammatory disorders and various carcinomas (May and Westley, 1997, *J. Pathol.* 183:4-7. pS2 is expressed in breast cancers (Poulsom *et al.*, 1997, *J. Pathol.* 183:30-38). pS2 is a pleiotropic factor involved in mucin polymerization, cell motility (Modlin and Poulsom, 1997, *J. Clin. Gastroenterol* 25(1):S94-S100), cell proliferation and/or differentiation, and possibly in the nervous system (see Ribieras *et al.*, 1998, *Biochim. Biophys. Acta.* 1378:F61-F77).

LIV-1 (SEQ ID NO:78) is an estrogen-regulated protein reported in the MCF-7 cell line (Green *et al.*, GeneBank submission Accession No. U41060). According to the present invention, LIV-1 is expressed in MCF-7 cells, but not in two metastatic breast cancer cell lines.

Leucine-isoleucine-valine -1 (LIV-1) and other members of the LIV family (LIV-2, 3, and 4) are binding proteins that represent a transport system for branched chain amino acids in *E. coli* as described in Yamamoto *et al.*, 1979, *J. Bacteriol.* 138:24-32, and Yamamoto and Anraku, 1980, *J. Bacteriol.* 144:36-44. A human homologue to LIV-1 is both estrogen and growth factor inducible in MCF-7 human breast cancer cell line (El-Tanani and Green, 1997, *J. Steroid. Biochem. Mol. Biol* 60:269-276; El-Tanani and Green, 1996, *Mol Cell Endocrinol* 124:71-77; and El-Tanani and Green, 1996, *Mol Cell Endocrinol* 121:29-35).

GTP-binding protein (SEQ ID NO:79) is a member of the family of guanine nucleotide-binding regulatory proteins, G proteins. The protein is expressed in MCF-7 cells, but not in two metastatic breast cancer cell lines.

G proteins provide signaling mechanisms for the serpentine family of receptors as described in Dhanasekaran and Prasad, 1998, *Biol. Signals Recept* 7:109-117. Studies indicate that the alpha as well as the beta gamma subunits of the GTP-binding proteins are involved in the regulation of several cellular responses, some of which responses are critical to the regulation of cell growth and differentiation (Dhanasekaran and Prasad, 1998, *Biol Signals Recept* 7:109-117). G protein coupled receptors regulate the mitogen activated protein kinase pathway as described in Russell and Hoeffler, 1996, *J. Invest. Dermatol Symp Proc* 1:119-122, and thus play a role in controlling cell growth. GTP binding proteins are also implicated in the regulation of intracellular transport as described in Ktistakis, 1998, *Bioessays* 20:495-504.

Chemokines induce various intracellular signaling pathways in natural killer cells by activating members of GTP binding proteins as described in Maghazachi and Al-Auokaty, 1998, *FASEB J.* 12:913-924. Heterotrimeric GTP binding proteins regulate distinct signaling pathways, some of which in turn regulate the activity of Na⁺/H⁺ exchanger proteins as described in Voyno-Yasenetskaya, 1998, *Biol Signals Recept* 7:118-124.

Desmoplakin (SEQ ID NO:84) is a member of a family of proteins that serve as cell surface attachment sites for cytoplasmic intermediate filaments.

Vimentin (SEQ ID NO: 80) is a member of the intermediate filament gene family (Evans, 1998, *Bioessays* 20:79-86. Intermediate filaments are a major component of the cytoskeleton of higher eukaryotes. Vimentin gene knockout mice indicate degeneration of the cerebellar Purkinje cells (Galou *et al.*, 1997, *Biol Cell* 89:85-97). Vimentin is positive in immunohistochemical reactions of sarcomas and related lesions (Gaudin *et al.*, 1998, *Am J Surg Pathol* 22:148-162), and of desmoplastic small round-cell tumors and their variants (Gerald *et al.*, 1998, *J. Clin. Oncol.* 16:3028-3036). Vimentin is also expressed in neoplasms showing follicular dendritic cell differentiation as described in Perez-Ordenez and Rosai, 1998, *Semin. Diagn. Pathol.* 15:144-154, and in biphasic carcinomatous-sarcomatous malignant mixed mullerian tumors as described in Guarino *et al.*, 1998, *Tumori* 84:391-397.

Cytochrome C Oxidase (CcO) (SEQ ID NO: 81) is the terminal enzyme of the respiratory chain of mitochondria and aerobic bacteria: it catalyzes electron transfer from cytochrome C to molecular oxygen, reducing the oxygen to water (Michel *et al.*, 1998, *Annu Rev Biophys Biomol Struct* 27:329-356). Cytochrome C oxidase is a member of the superfamily of quinol and cytochrome C oxidase complexes that are related by a homologous subunit containing six positionally conserved histidines that ligate a low-spin heme and a heme-copper dioxygen activating and reduction center as described in Musser and Chan, 1998, *J. Mol. Evol.* 46:508-520. Cytochrome C and ubiquinol oxidases are membrane-bound redox-driven proton pumps which couple an electron current to a proton current across the membrane (see Karpförs *et al.*, 1998, *Biochim Biophys Acta* 1365:159-169). Analysis of mutant forms of cytochrome C oxidase is described in Mills and Ferguson-Miller, 1998, *Biochim Biophys Acta* 365:46-52. Nitric oxide inhibits respiration at cytochrome C oxidase, as described in Torres *et al.*, 1998, *J. Bioenerg Biomembr* 30:63-69.

Heat shock protein 90 (hsp90) (SEQ ID NO: 82) acts as a chaperone molecule in association with the glucocorticoid and progesterone nuclear receptors, and has A, B, and Z regions for facilitating these interactions (Dao-Phan *et al.*, 1997, *Mol Endocrinol* 11:962-972). Levels of hsp90 are reported elevated in active systemic lupus erythematosus (Stephanou *et al.*, 1997, *Biochem J* 321:103-106). Increased hsp90 expression is implicated in regulation of forms of cell injury that lead to programmed cell death as described in Galea-Lauri *et al.*, 1996, *J. Immunol.* 157:4109-4118. Hsp90 is upregulated in regenerating fibers and diseased fibers of Duchenne muscular dystrophy (Bornman *et al.*, 1996, *Muscle Nerve* 19:574-580), and is a candidate substrate for proteolysis during ionizing radiation-induced apoptosis of some breast cancer cells (Prasad *et al.*, 1998, *Int. J. Oncol* 13:757-764). Hsp90 is involved in dislocation of the mutant insulin receptors from the endoplasmic reticulum to the cytosol as described in Imamura *et al.*, 1998, *J. Biol. Chem.* 273:11183-11188, and associates with and activates endothelial nitric oxide synthase as described in Garcia-Cardena *et al.*, 1998, *Nature* 392:821-824.

Integrin alpha 6 (SEQ ID NO: 83) is in the family of integrins, heterodimeric, cation dependent cell membrane adhesion molecules that mediate cell-cell and cell-matrix interactions. Integrin alpha 6 is a component of the hemidesmosome complex (Jones *et al.*, 1998, *Bioessays* 20:488-494). Integrins
5 maintain tissue integrity and regulate cell proliferation, growth, differentiation, and migration. (See Thomas *et al.*, 1997, *Oral Oncol* 33:381-388). In oral squamous cell carcinomas there is a variable loss or reduced expression of integrin alpha 6, as described in Thomas *et al.*, 1997, *Oral Oncol*, 33:381-388. Alpha 6 integrin also plays an active role in invasion of intestinal and diffuse-type cells of representative gastric
10 carcinoma cell lines as described in Koike *et al.*, 1997, *J. Cancer. Res. Clin. Oncol.* 123L:310-316.

Osteogenic protein-1 (OP-1) (also called BMP-7) (SEQ ID NO: 85) is a morphogenetic factor (and a member of the bone morphogenetic protein (BMP) family of growth factors) and is highly expressed in kidney and involved in tissue repair and
15 development (see Almanzar *et al.*, 1998, *J. Am. Soc. Nephrol.* 9:1456-1463). OP-1 is also expressed in the developing nervous system and can induce dendritic growth in sympathetic neurons as described in Guo *et al.*, 1998, *Neurosci. Lett* 245:131-134. OP-1 stimulates cartilage formation as described in Klein-Nulend *et al.*, 1998, *J. Biomed. Mater. Res.* 40:614-620.

20 OP-1 induces down-regulation of insulin-like growth factor binding proteins (particularly IGFBP-5) thus affecting IGF-1 in the context of bone cell differentiation and mineralized bone nodule formation as described in Yeh *et al.*, 1997, *Endocrinology* 138:4181-4190. OP-1 can be used as a bone graft substitute to promote spinal fusion and to aid in the incorporation of metal implants (Cook and Rueger, 1996, *Clin. Orthop.* 324:29-38). The three dimensional structure of OP-1 is reported in
25 Griffith *et al.*, 1996, *Proc Nat'l Acad Sci* 93:878-883.

The protein encoded by SEQ ID NO:56 is a putative secreted protein and is highly expressed in fat tissue.

Table 1. Novel Differentially Expressed Metastatic Marker Polynucleotides

TRANSCRIPT NUMBER	SEQ ID NO:	non- metastatic breast MCF-7	breast cancer metastatic to bone and/or lung MDA-MB- 231	breast cancer metastatic to lung MDA- MB-435	low metastatic from colon KM12C	high metastatic from colon KM12L4A
901	1	-	+	-		
907	2	-	-	+		
9102b	3	+	-	-		
9114	4	-	-	+		
9121a	5	-	+	-		
9129	6	+	-	+		
9139a	7	+	-	-		
9143b	8	+	-	-		
9157b	9	-	-	+		
9166	10	+	-	-		
9170b	11	-	+	-		
9190a	12	+	-	-		
9191	13	-	-	+		
9216	14	-	-	+		
9224c	15	+	-	-		
9230b	16	+	-	-		
924	17	+	-	-		
9242a	18	-	+	-		
9259a	19	-	-	+		
9261	20	-	+	-		
9272	21	+	-	-		
9293b	22	-	+	-		
9304b	23	+	-	-		
9307a	24	-	-	-		
931	25	+	-	-		
9313	26	-	-	+		

TRANSCRIPT NUMBER	SEQ ID NO:	non- metastatic breast MCF-7	breast cancer metastatic to bone and/or lung MDA-MB- 231	breast cancer metastatic to lung MDA- MB-435	low metastatic from colon KM12C	high metastatic from colon KM12L4A
9316	27	+	+	-		
9318b	28	+	-	-		
9320a	29	-	-	+		
9330b	30	-	+	-		
9335	31	+	-	-		
9337	32	+	-	+		
9342b	33	-	+	-		
9343c	34	+	-	-		
9350e	35	-	+	-		
9351b	36	-	+	-		
9361	37	+	-	-		
9368	38	-	+	-		
9373b	39	-	-	+		
9385a	40	-	-	+		
9386c	41	-	-	+		
9388d	42	+	-	-		
9390	43	+	-	-		
9393	44	+	-	-		
9396	45	-	+	-		
944b	46	+	-	-		
951	47	+	-	-		
953	48	-	-	+		
954a	49	+	-	-		
968	50	+	-	-		
971	51	+	-	-		
983c	52	-	-	-		
985	53	+	-	-		
990	54	+	-	-		

TRANSCRIPT NUMBER	SEQ ID NO:	non- metastatic breast MCF-7	breast cancer metastatic to bone and/or lung MDA-MB- 231	breast cancer metastatic to lung MDA- MB-435	low metastatic from colon KM12C	high metastatic from colon KM12L4A
998	55	-	-	+		
316	56	+	-	-	+	-
126c	57	-	-	+		
207-4	58	-	+	-		
265-3	59	+	-	-		
29B	60	-	-	+		
305B-25	61	+	-	-		
326B-39	62	+	-	-		
34B-11	63	-	-	+		

+ indicates differential expression as identified in differential display

- indicates absence in differential display

For transcript number 316, reverse transcription PCR (RT-PCR) was
5 used to detect expression in the breast cancer cell lines.

Table 2. Differentially Expressed Metastatic Marker Polynucleotides

TRANSCRIPT NUMBER	protein	SEQ ID NO:	non- metastatic breast MCF-7	breast cancer metastatic to bone and/or lung MDA-MB- 231	breast cancer metastatic to lung MDA-MB- 435
902	osteopontin	64	-	-	+
9112	nip	65	-	+	-
9132	Ca-dependent protease	66	-	-	-
9158	IGF-R	67	-	-	-
9174	ILGF-BP5	68	-	-	-

TRANSCRIPT NUMBER	protein	SEQ ID NO:	non- metastatic breast MCF-7	breast cancer metastatic to bone and/or lung MDA-MB- 231	breast cancer metastatic to lung MDA-MB- 435
9177	lactate dehydrogenase	69	-	+	+
9202	ufo TKR	70	-	+	-
9210	eIF2	71	-	+	+
9212	glutaminyl cyclase	72	-	-	+
9213	gp130	73	-	-	+
9222	TGFb-II	74	-	+	-
9232	E-cadherin	75	+	-	-
9239	serpin	76	-	+	-
9250	secreted pS2	77	+	-	-
9260	LIV-1	78	+	-	-
9315	GTP-binding protein	79	+	-	-
9317	vimentin	80	-	+	-
938	cytochrome C oxidase	81	+	-	-
9382	Hsp 90	82	-	-	+
9394	integrin a6	83	-	-	+
956	desmoplakin	84	+	-	-
970	osteogenic protein	85	+	-	-

+ indicates differential expression as identified in differential display

- indicates absence in differential display

Within the scope of the invention are variants of the proteins described
 5 above. A variant is a protein encoded by a polynucleotide wherein the global sequence
 identity of the DNA, as compared to the corresponding SEQ ID NO: herein, is at least
 65% as determined by the Smith-Waterman homology search algorithm as implemented

in MPSRCH program (Oxford Molecular) using an affine gap search with the following search parameters: gap open penalty of 12, and gap extension penalty of 1. The protein encoded by the DNA having the sequence identity described above will exhibit the percent activity described in the preceding paragraph.

5 Also within the scope of the invention are fusion proteins comprising the proteins and variants disclosed herein. Proteins preferably used in fusion protein construction include beta-galactosidase, beta-glucuronidase, green fluorescent protein (GFP), autofluorescent proteins including blue fluorescent protein (BFP), glutathione-S-transferase (GST), luciferase, horse radish peroxidase (HRP) and chloramphenicol
10 acetyltransferase (CAT). Additionally, epitope tags are used in fusion protein constructions, including Histidine (His) tags, FLAG tags, influenza hemagglutinin (HA) tags, Myc tags, VSV-G tags, and thioredoxin (Trx) tags. Other fusion constructions can include maltose binding protein (MBP), S-tag, Lex A DNA binding domain (DBD) fusions, GAL4 DNA binding domain fusions, and Herpes simplex virus (HSV) BP16
15 protein fusions.

 These fusions can be made by standard procedures in the art of molecular biology, and many are available as kits from, for example, Promega Corporation (Madison, WI); Stratagene (La Jolla, CA); Clontech (Mountainview, CA); Santa Cruz Biotechnology (Santa Cruz, CA); MBI, International Corporation (MIC,
20 Watertown, MA); and Quantum Biotechnologies (Montreal, Canada).

 The proteins of the invention, and variants as described herein, can also be used to detect protein interactions in vivo, using the yeast two-hybrid system, for example as described in U.S. Patent No. 5,674,739.

 In addition to the ribozyme and antisense constructs described above, the
25 polynucleotides of the invention can be used for inhibiting transcription via triple helix formation as disclosed in U.S. Patent No. 5,674,739.

 Those skilled in the art will recognize, or be able to ascertain, using not more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such specific embodiments and equivalents are
30 intended to be encompassed by the following claims.

All patents, published patent applications, and publications cited herein are incorporated by reference as if set forth fully herein.

CLAIMS

We claim:

1. An isolated and purified human protein comprising an amino acid sequence which is at least 85% identical to an amino acid sequence encoded by a nucleotide sequence selected from the group consisting of SEQ ID NOS:1-63 or the complement thereof.
2. The isolated and purified human protein of claim 1 wherein the amino acid sequence is at least 95% identical.
3. The isolated and purified human protein of claim 1 wherein the amino acid sequence is encoded by a sequence selected from the group consisting of SEQ ID NOS:1-63 or the complement thereof.
4. A fusion protein which comprises a first protein segment and a second protein segment fused to each other by means of a peptide bond, wherein the first protein segment consists of at least six contiguous amino acids selected from an amino acid sequence encoded by a nucleotide sequence selected from the group consisting of SEQ ID NOS:1-63 or the complement thereof.
5. A preparation of antibodies which specifically bind to a human protein which comprises an amino acid sequence encoded by a nucleotide sequence selected from the group consisting of SEQ ID NOS:1-63 or the complement thereof.
6. A method for detecting metastatic tumor cells in a tissue sample, comprising the step of:
measuring in said tissue sample an expression product of a gene which comprises a coding sequence selected from the group consisting of SEQ ID NOS:1, 2, 4, 5, 9, 11, 13, 14, 18, 19, 20, 22, 24, 26, 29, 30, 33, 35, 36, 38-41, 45, 48, 52, 55, 57, 58, 60, 63-

66, 69-74, 76, 80, 82, and 83, wherein a tissue sample which expresses the product is categorized as containing metastatic tumor cells.

7. The method of claim 6 wherein the expression product is protein.

8. The method of claim 7 wherein the protein is measured using an antibody which specifically binds to the protein.

9. A method for detecting metastatic tumor cells in a tissue sample, comprising the step of:

measuring in a tissue sample an expression product of a gene which comprises a sequence selected from the group consisting of SEQ ID NOS:3, 7, 8, 10, 12, 15-17, 21, 23, 25, 28, 31, 34, 37, 42-44, 46, 47, 49-51, 53, 59, 61, 62, 67, 68, 75, 77-79, 81, 84, and 85, wherein a tissue sample which does not express the product is categorized as metastatic.

10. The method of claim 9 wherein the expression product is protein.

11. The method of claim 10 wherein the protein is measured using an antibody which specifically binds to the protein.

12. A method for determining metastatic potential in a tissue sample, comprising the step of:

measuring in a tissue sample an expression product of a gene which comprises a sequence selected from the group consisting of SEQ ID NOS:1, 2, 4, 5, 9, 11, 13, 14, 18, 19, 20, 22, 24, 26, 29, 30, 33, 35, 36, 38-41, 45, 48, 52, 55, 57, 58, 60, 63-66, 69-74, 76, 80, 82, and 83, wherein a tissue sample which expresses the product is categorized as having metastatic potential.

13. The method of claim 12 wherein the expression product is protein.

14. The method of claim 13 wherein the protein is measured using an antibody which specifically binds to the protein.

15. A method for determining metastatic potential in a tissue sample, comprising the step of:

measuring in a tissue sample an expression product of a gene which comprises a sequence selected from the group consisting of SEQ ID NOS:3, 7, 8, 10, 12, 15-17, 21, 23, 28, 31, 34, 37, 42-44, 46, 47, 49-51, 53, 59, 61, 62, 67, 68, 75, 77-79, 81, 84, and 85, wherein a tissue sample which does not express the product is categorized as having metastatic potential.

16. The method of claim 15 wherein the expression product is protein.

17. The method of claim 16 wherein the protein is measured using an antibody which specifically binds to the protein.

18. A method of predicting the propensity for metastatic spread of a breast tumor preferentially to bone or lung, comprising the steps of:

measuring in a breast tumor sample an expression product of a gene which comprises a sequence selected from the group consisting of SEQ ID NO:1, 5, 11, 18, 20, 22, 24, 30, 33, 35, 36, 38, 45, 52, 58, 65, 66, 70, 74, 76, and 80,

wherein a breast tumor sample which expresses the product is categorized as having a propensity to metastasize to bone or lung.

19. A method of predicting propensity for metastatic spread of a breast tumor preferentially to lung, comprising the steps of:

measuring in a breast tumor sample an expression product of a gene which comprises a sequence selected from the group consisting of SEQ ID NOS:2, 4, 9, 13, 14, 19, 26, 29, 39-41, 48, 55, 57, 60, 63, 64, 72, 73, 82, and 83.

wherein a breast tumor sample which expresses the product is characterized as having a propensity to metastasize to lung.

20. A method of predicting propensity for metastatic spread of a colon tumor, comprising the steps of:

measuring in a colon tumor sample an expression product of a gene which comprises the nucleotide sequence shown in SEQ ID NO:56,

wherein a colon tumor sample which expresses the product is characterized as having a low propensity to metastasize.

SEQUENCE LISTING

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 cctttacagg tcctgggggtc caggagaccc agaalgagg tgtcagttgg gcatgaagt 180
 tta 183

<210> 5
 <211> 1092
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(1092)
 <223> n = A,T,C or G

<400> 5
 ttncagacca agaagacttg atnagctgaa acccattgcn ctacttggaa ngtgatngc 60
 aaaagctgcc tcagtcnanc accgggggata aactctggatt tgggttcgg cgicaaggtg 120
 aanatnatac ctantaanga acnctgtaca ntgcncnag cangtganga cncccacga 180
 gttacatna atacaatnct gaaacnanc aggtctggtt tatatctaca taittgactt 240
 accactatcn cantaaagt tngcaccttt cncggaacga aaanaacccc cctnnngnn 300
 ttcttttnaa aanacnctng nncnctnn cgcgcncc cennatantn ncnatccc 360
 cccctctncc nntcctnnn cgtaanaggg gngctctng cngtntngt cccgtttcc 420


```

tccgcttngt cntttntcta tatnggctnn tnttatneen ngcccttctg cncctnnngn 480
tccgtctgtg cntagtcctc ntctctngag cccanttgnt acttcnngct tcnctccgc 540
altcentctc cgenennanc ncnntctca nannatgnnc nntnctnnc ncnatnnc 600
cctnanagnt tcgctagac cntenacntt gtntcccggn ctcttagngn tctgctncta 660
gtgtntnct catctctct ncttctctct cctttagcnc ngnnctctcc atctnttct 720
gnctttctca tcnctnnng cccctnctcn cnnagtntgn gtgenennnc ttnnnntena 780
nctngtcgcc tccgttttct actnnnnccn nngcngnng nngctctctt ctntcnntta 840
gactnacctt nctggnnnnn tcannctagc nctgtccctc tctntctgc atcttanac 900
atctnnntcn cccnctcgca nctnctntt nacnctcnca tacgttneen nctcagtc 960
gcagnnngt tcnctnngt cntctcgcgn ctennntct ctctnnnacn cncctggtct 1020
nctnctctct cccncccatn cntnctctgt tgnctnnnt cnnatacgt tncangcnc 1080
ntctctcnc tn 1092

```

```

<210> 6
<211> 504
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(504)
<223> n = A,T,C or G

```

```

<400> 6
ctggagcggg atcatttana atactttaca gatatntgca ccaggtacat ntatntgct 60
ccattggtag cacagctgag acctgtgtct cacatcagc taggtgaagc ctactacaaa 120
taatgccaag ggagaanagc cagtacacta tatggtttat actctttatc cctttattca 180
tagcalgttt tttaaaaatg ttatattatg caacagatgt gaggcagcan ctaagctata 240
cttaagaatt ttctctcac ttccaaacca aagtgtcttg aataagccag gagacttatt 300
cttttgtgca cctggttgca catctgactg ttgtctanc canaaactct ctgagggcac 360
tgaaagaaca gtggccctat cgatttcatt cctaggtctc aaaaatacna tgtngccttg 420
taacataatt agggacagca cctctatttc acaattataa tctaaggtag gataagacga 480
cacagcagca ataaacttac aagt 504

```

```

<210> 7
<211> 1132
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(1132)
<223> n = A,T,C or G

```

```

<400> 7
gcgngccccc tngtngnnn tntnctnng tttctgctn tnttatnng aggnctnggt 60
nnttntctt agggnnntng tncggtcnng ttnntgttnc gagcagaaag tgnatatttc 120
atgngcccaa gcttntttat tgaaaantcc taattntatt gncgnttag taacatgttt 180
gttcracaan gctaatttct nataaancaa aacacannnt tttcttataa gtngtataaa 240
ttallnatc tacagaaact tgtttcaaaa canatgnact anntatttct nctcttttaa 300
atanccanac taattttcta tccctngaca tctgttcctg ttctatnag cagccaacac 360
aaagtccanc tgagagctct tgattaangt gtnegratta tctagctact tccnagcttt 420
tngngcnng aaatgnttt taanancttg gctcaaaaa anaaaaanan cccccggnn 480
aggggnnttc cntntaaaa aanggtctc tcnctngtn ngagactgtc tccctgnttn 540
ngnnntctg tntnatcang ngcncnang ctncntcn ctnnngcatt ngatnnntan 600

```

```

cnnnctgaga tgnnntang ctgntnctn ngtgtcttan gtctcgacgt tgnntggntn 660
tangnanacgn cnnntnnc nnattgncga gngnntaagt gtgctcttct cntnactct 720
ntcnnnancn tctnnatgt tnatcggcc gtgcttctt atcnntgana ncgntctnan 780
nannlnacna tgagntnta ctgcnctnt gtgtcatctt tctctctant gtgtctnna 840
nncnngtnat tncgcnnaac tgnatnag tggatnnag anntcgnncg cngngccnn 900
tttntctgt gnatnagnt ntcanganat tnatcnctc tncgtgalag anagntnagt 960
gngngntctg actgatnct gtctagttn cngtgacatc gnnctgtann gtengcactc 1020
tagtanant nagtnngang ntgtanatn ntctctgtt tcagtnnagn cccnccgagcg 1080
cntcanntnt nantgtctcn tctnnctgt annctgtctg agtnngtnana nn 1132

```

<210> 8

<211> 736

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(736)

<223> n = A,T,C or G

<400> 8

```

ntgggcccga cgtcgcatgc tcccggncgn catggnnnc tggtttggtc anatgtgaat 60
aacgnagaan tgagaccacn ganaagaacc acantgtan ggnccttgca cntgntanga 120
antnagnaat gccttttnc tgaggcctt nggnntcat nnangggngt gngnggntt 180
ncacctgtaa taccaccact ttncnatgcc actgccngtg natcacnng ngtaaggact 240
tcaanaccag ccttatnaac ntgggnaaac cntntctc ctaaaaatnc tnaantatc 300
tgngcnngt ngngcgttct tntannccn gctgnacnng angncngng angntantcg 360
cntgaactg ncntgttana gtngcantga gcctaaatca cantgatgta ttncatctg 420
ggacgacacg ancgacgac tncgtactn aaaaaaaaaa ncccttng ggggggttt 480
ttnnggtatt anntatant ggagaanttt gggtcannng aatattnta catgaaaaat 540
naggaataac tntatntgtg tacattgggt tnaaanang acantantgg nctaaactn 600
ttngggngg aggggnatt agggnttaa ttngnnct tnaaanncn ntnngtat 660
nanaanantn tttnnanaag ngnantngt taaancctn aangnttnn tctnttann 720
ttnaannnn anann 736

```

<210> 9

<211> 690

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(690)

<223> n = A,T,C or G

<400> 9

```

tnnccctggg tggcactcc cttctgtcct gttagctcat ggtgtaagal gatgtctgt 60
cagtattact gttttgctaa gccgcttcat tcatgcctac acaatttttt tttaaaagg 120
aactttagt aattaagtga taagggaactt aaatatgaat tanaatggtg cagaagaga 180
tacctttct ggatatttla aggttlaaag gtcantttct cttaactctga ttatgtgcac 240
atatgaaaat ggcacatcat atacatgtaa aatcaggcag tatncattla ttaattactg 300
tatitgacaa aggaactct taaattataa tgtgaaacct ggttttatga aaccaatgac 360
tagtgcanca tttcagcata tgcaaaaaaa aaannccnt tggngngctg ttacaaagg 420
aaattgttg atttcacgat ggttcagga naanaaggtt tctctcatc agggtaaacn 480
tcccggataa ggcnngntt taatntntt annccnccn atngntaann gtggaaatta 540

```

```

ancctctgaa naaaanance cacntnnttn gccttgggct tnantctntt tggcngnanc 600
naaagggnct tncaggtnt cntgnngggc cngnngaann ataannaann nggggnnctt 660
nggaaacctt ncnnaanan tcccccccc 690

```

```

<210> 10
<211> 395
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (395)
<223> n = A,T,C or G

```

```

<400> 10
tggatcttga cnaataaga atgcacccat ttgtgagggg taatatattat ctcangattt 60
actgtaaaata tgtatacaca catacaaaaa cccaggcatt gttaaagagaa aatnatggcc 120
cagaggttna aattatcaga cagaaccttt aanaataatt atgattaatg tgttaaaatt 180
ctagtggaaa agataaataa catgctcagg anatttttagc anagagatag aaactatntn 240
ngaagctcaa atgaaaatgc taggaaatga aaagcagtat tggaggtgaa agattccttt 300
ggcaatttat caacanactg gagatggcan aggcataatc agtantattg aaggcagatt 360
actaintatt atncaancaa aaaaaaaaaa cccct 395

```

```

<210> 11
<211> 331
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (331)
<223> n = A,T,C or G

```

```

<400> 11
aacgagggcn ngaggccaat gaggccaaca agacgatgcc ggagacccca actggggact 60
cagaccogca acctgctcct aaaaaaatga aaacatctga gtccctcgacn atactagtgg 120
ntcgctacag gagggaaagt gaaaagaaca tctccagagg aactgggtgaa tgaccacgcc 180
cgagagaaca gaatcaaccg cgaccaaagt gaggaggagg aattcataga aataacgact 240
gaaagaccta aaaagtagca agaagctaca tccctcaaac ttcggcaatg aaaataaagt 300
ttgagaagct caaaaaaaaa aancctttt g 331

```

```

<210> 12
<211> 693
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (693)
<223> n = A,T,C or G

```

```

<400> 12
tncacgcgt tgggagctnt nccaaggtgg nctagcnnda ttaatgcctt accgtgggaa 60
tatggntgaa gatcttgact aggggactta tgaacccatg cagccgtgcc caaatcctac 120
caactgacc ttactttctt gaagacggaa ttgtagtatg gtctagctca tgctttttgt 180

```

```

agtagggccat ncaaattcga ttgactggct aaaaaagatt gttagtggag gctggaagaa      240
acatttltggc tgatgataga tgaatagagc ttggaacaat caaaaggaaa agcagaaagt      300
ctatacctat tcataagaaa aagttagtat gttaccgaa cattatnaaa gaattatgac      360
attttcaaag ttttaaaatt ttattttgta gggacggggg ctcattgtgt agcccacnct      420
ggctctgtttc ttgaggattt actatanact gggctgtatt caaagcattg gggatacagg      480
catgaatgag cccccattgc ctgaacttac cattcaatct gggcagtga agaanaaggga      540
tgntgggaga nccttacaac gatgaaalgt cgctaactgg agaaatccct actttcagtc      600
agactgaann ggaacaggta gtnactgtgg gtagccctct ttgggnangg gtngattttc      660
cacatgtgcc cagttaaggg ccnagaacat taa                                     693

```

<210> 13

<211> 305

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(305)

<223> n = A,T,C or G

<400> 13

```

ttggtatcng gggatgggng aggggagata gncccgaagc atcccnatt ctcaagaaac      60
tccttggnat canannatat cntggccnaa gaaccnncna cctctctnng gttagaaata      120
ccgctntatn gngtatgagg ggaatngggcn tacgnnataa ttttctatng ganggtattn      180
ccgcactant gacnagttct ttctnnggic calttnnaac nacantnttg acattgntga      240
tctgcaannc tgtaaaatag tcttncagtg ggcaatnnnt gcacaactgg gttnggtntc      300
anaca                                             305

```

<210> 14

<211> 308

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(308)

<223> n = A,T,C or G

<400> 14

```

agcagacaac ntaatccaag ccatttacca aataantata tgcgatgcac attgaatcct      60
ggcgctctag atatantgcc ccaaaggaaa gagnaacaaag tnttcnccc ntagttctac      120
natgnctatc cncatcacc tncgtnttcn naagnlttnt aaaaataaat tctcttgtat      180
ancatccnat atncaccgg tccaaagcgc aacaatctgc aattcanaan ttccaacaat      240
cnahtatgn actttctag gtccggtgtt ctaanatnla atattctaac acttactctc      300
agatctta                                         308

```

<210> 15

<211> 304

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(304)

<223> n = A,T,C or G

```

<400> 15
ngt naaggga tatttattcc tgttttaaaa ggatacaacc aaggtaggga aggccttcgtt      60
attgggtgatt attcagaaga cctattttct ttacatatgc tatggaaaca atactgtttt      120
ccgctacaga alacagltta tgattatact tttgtaaatt gcctgctttt cccctgtcat      180
ctgctaattc caatttgata ctgttctgtg ttcaaaaata cagcatgagc aagctgtaal      240
ggtgcctgtc gagagtccca gctgcttggg gggctaaggt gggaggatca tttgagccca      300
ggag                                          304

```

```

<210> 16
<211> 703
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(703)
<223> n = A,T,C or G

```

```

<400> 16
ccggtngnct aaaaaggacc agcctaattgt agaaggtggg tatttggacc agaggcttta      60
gattattatt ttagatccta catatacttt tatcagtaga atgatttcat tnagatgtat      120
aatgaaaaag ggtaatgcaa aaattatgta atagalacca aattagggaa gtttggcaat      180
ttcaatggca tatttttagt caaggnacac agatggcagt gccataagca agtctataaa      240
tatcggtgc agccatcccc ctcatthtaaa atgttgccct aataatcaat gcagttaaca      300
agtatatlgg ctgtgtgtca tgaaatagtt catgttcaga tggaaatggt aggttactgt      360
atggtttatg gagattaatg aaaatgaatg cccaaaaaaa aaannccntt tngngngngg      420
tttnnnangn acngggctgg attcaaanca tlggggatnc angnttnaat gngnccccat      480
ttgnctnaac ttaccttnna nnttgggcnn tnnatngaen angggatnnt gggannaacc      540
tttnnangnt nnaantglnn ncttactggn gnaaannncc ntaanntttt nnnntnnnnn      600
ngnaangggg naannnnnnn ntnancttnt gggggagnen nttntggggn anggggggnt      660
nnttnnnnnn tnnnggcenn nnnnggggcn nnaaantttt tgn                                          703

```

```

<210> 17
<211> 171
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(171)
<223> n = A,T,C or G

```

```

<400> 17
tccgntcta agtaattcat caataacgca tgtccactta atgtgaaaat tggtagcatc      60
taatanaalc ttcaacatgg cnatccacnc tattccaata atgaaatgca aatttcctg      120
ccttctttac tanggtcatt tntagattct tgaggaaatga gttctactct t                                          171

```

```

<210> 18
<211> 689
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature

```

<222> (1)...(689)

<223> n = A,T,C or G

<400> 18

```

antnngcttn ggtactaagc agaatcactt ncttgggaac tccatgtaac tngtggcttt      60
tgtgattgaa atagcatcag taaangtctg acctgtggg aaagacacat atgnngctgg      120
accnggctat gtctgacttt gtgctgctca ggacactctc tgnaccaaa agngagagan      180
cctggannac ctcanggggt canatgtttg aaggagctgc tgagtatcct ggcaggcanc      240
anagccttac catcagtttg ctgcatggaa ggctgtgtgc ctctalltcc ctgctatttg      300
ttgaactccc ttgagctccg gtccttccca agtgagagag atgatcccaa tagcnccaac      360
ctgagagggc tggggagatg ttngaaggaa agcttggctg gggagctgaa tctggcctgt      420
ggtacatgct tggtaactgg tggccaggan acccgggngt gtgtnctggg actgtcncac      480
tctgctgacc aggggtattga aagtcgccnc tcaaanacac agaattntnc tgaccaaggg      540
tangtatgan atgacntgtg gagcactttg nataaactgg ttctcatnng nggtcccttt      600
gaanaggtgc tnnatctgtt caaaaatacg tggctgagct ntanacceng natcctctgt      660
cagagacatg ggcaggggga ctcaatgct                                     689

```

<210> 19

<211> 721

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(721)

<223> n = A,T,C or G

<400> 19

```

latanatact nngctatgct ttctaccctg tgtgcctgga gacctactat ggaaaaanga      60
tcagccacct taccttctac tgggtacctg ctgtgagctt gcctatgcca caacgattaa      120
tgangggagg gtaccaagn gacaaanccn acatgccgct tacagccccc gttggalnng      180
tgetcattca acagtcttgc attcagtagg tgtttgacat caccclactat gtgncagget      240
ctatgctang nactggggat acaggagaga nlnaagcgta aagtctttgg tctcaaggaa      300
tttgcatlct agaaagtcta agatgtaata aatgtactgt gggacatgtt aaataagtgct      360
lataacgaaa tataaagggt ttgggagcaa aaaaanaacc cnnttggtgg gntctntncc      420
nctctgatga agcttactta cttttaacct tnccttctcc tttaaagggt tttcctgggt      480
ccccttlect ttacagattg gttattggct ttgctgagga gtaggactac aattnccagc      540
attctnctgg aagccaaagc tgtgctacaa ttgnnccaaa gaagatngta atcttaagcg      600
ccntaatgg taaaatngta ttaaaangtg gacctttgac aaataaattg ntctgatllc      660
ngaattccgg gttngnagct lngnynlncc aaaaaccctt nggggntccc ttttgggcac      720
c                                                                                   721

```

<210> 20

<211> 248

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(248)

<223> n = A,T,C or G

<400> 20

```

cttaaacacc cccccactc nccccccaga atgagnlaan cataactctc nntactgnat      60
ctccglatcc gtcctacnc nggnttgta ggtgtcatta gongatatta ctccctacn      120

```

```

ncatcntgan cannatcccc catcncccat atgntgatna nnacaaacca tncatattncg      180
ccgngaagc cnnctnnttc attggattcn tagaccgcan angtcctnat tcngacacng      240
aatcggtgta                                     248

```

```

<210> 21
<211> 298
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(298)
<223> n = A,T,C or G

```

```

<400> 21
ggctctaaggg atgtgatgng agcatagaat ttancntat ggncatanta gggacatntg      60
ctgatntacn tggncctgcgg tcnntgaaag gtggngnatg atgactgatg tcatnagtag      120
tacnanggac tncgnnanct gggatcnggg nttacnttgt tcatngtnag agtgnnanen      180
aagtanatgn taggnataaaa gatgttncgg gagatgggtc taaaaantct tttnaagatg      240
ntcatcttga anannatcaa gtgtgnttgg tataatgact atcattatac aatgtcaa      298

```

```

<210> 22
<211> 591
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(591)
<223> n = A,T,C or G

```

```

<400> 22
tcgctagani actattcggc cgcaacgggg agcctgatga ggacgcttat gatatgagga      60
aagcactttc cagggatact gagaagaaat ccatacacc attacctcat cctgtgaggc      120
ctgaagacat tgaataacc tgggcagtgg ttcllaggca gatactctag atgctttatg      180
gacaatatta ttttcatttg atgattcttg agctctatta ggagaaaagt aatcatltta      240
ggctctaaag acttcaagaa aatacagggt atcaatttat tllaaalcic attgtttcca      300
gttagcaata tcatacctat taaagctgtt cattgtaaca aaattcaatc aaaaaggcag      360
ctaggtcaga aggaacata ccactctcat gggtcatagt attcactgta tgtatgctag      420
ggaaaagact tgcctcagtc tctcctcag ttctgtgcct gagaaccact gctgcatata      480
tttgttttta aattttgtat tgaactgtta attgaagctt taaaagcata tatgaaatgt      540
ataaalclaa gatgtataat acattattga ctccaaaaaa aaaaaccctt t      591

```

```

<210> 23
<211> 755
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(755)
<223> n = A,T,C or G

```

```

<400> 23
gnnnnnnggt rnnnagcngg ttnggtncng actccenttt atnatgaggg acactgaggg      60

```

```

ttcaagagat taggagactt gttcaaagac acacagctgg taagtgatgg aggcaggatt 120
taaacctggg ttctactgca ttcccatca ctggctttta gccatgatgc tctactgtgt 180
aaccctctta attcttgacc tgtggctata aagtatgtat tgagagacag gccctccctg 240
agataacttt ccagccttga caaaggcaca cccttgggtc attccttggg gtgtaggacc 300
tagattgtga caagcccaga tgaglgltgc tggcagaggg gagcagatct gaggccacca 360
tatgtgttca cctagcccta aggagtgccg gcttcgctgg tatttgtaca gcttccatca 420
ggactgctca ttggccacgt tcttccctct ccctgccacg ttgattaata ctccacataaa 480
ttaatgctca cattagtgtt caagtatgca aatgagtgtt taaaatcatc actcacacaa 540
tgaccagact gaggatataa cacacaagag cccctctcct ggtaacccca caatcatgca 600
gatgtgttga cttctctgca ttaccagtct ggtaggcagg gggatatgac agttagaaac 660
agtctttcan acagcagttc tcaacaccag gtcccttgcg gcacaatcga atcacctggg 720
ggtttaaaaa aatatcatgc cagtcagcca cnntt 755

```

<210> 24

<211> 513

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(513)

<223> n = A,T,C or G

<400> 24

```

ctttctaccc aacaagcata gaatatacat tgtatacatc agaaacacgg gacattctcc 60
aaaatagacc atatgatagg gcacaaaaca agtctcagta aatttaagaa aatcagaatt 120
atatcaagta ctctctcaga ccacagtggg ataaaattgg aaattaattc cgaaagggaac 180
actcaaaagc atgcaaatac atggtaatta aataacctac tctgaatga ttgttgggtc 240
nacaatgata tcaagaggga aatttataaa ttctttgaac tgaacgataa tagtgacaca 300
gcctatcaaa aactctggga tacagcaaaa gtggaggtaa gaagaaaatt catagcatta 360
aatgcctata tcaaaaatct gaaagagcac aaataaacaa tctaagggtc ccctcncaga 420
attggagaaa ctagaacagt ccaaatccaa acccngcaga agaaaagaaa taaccaaact 480
cgaacaaaac taaatgaatt gaaaaaaatc ccc 513

```

<210> 25

<211> 574

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(574)

<223> n = A,T,C or G

<400> 25

```

cgatccaaga gattagaanc cntggagtg gagcatgctt cncatanaatn ccacctgatn 60
cttggctnaa nacantrngc tctantttgc tttgtgcccg tccacacaan ctaaaaacaa 120
gggatggggg gacncnagc gtctaataatn cntaataatc ntcncnggc aaatgaatac 180
tttttacaca cttgtanntt ntggagggan ggggtnatna tgaggggaan gggaaaggat 240
gaggagaaat ccaggatnan angctcttc gtctctcna gaetnctca cactctntgt 300
ggtnaccngg gttcgttnlg tccaatggca gacattatac tccatantct acccnggctt 360
nntcgggttg ggacgccann actccccna gtngtnncc cenanacagc atacacaagt 420
ntgaacgggt tttgtggcca ntcatcgcaa tgacctntc etcnactcna agaaaantaa 480
acccctctcc ccngattggg ttctaaatct ttccacctat ctaaaataga aagcncnag 540
tgggaggggt tnatccccc ntacccntta aaac 574

```


<210> 26
 <211> 185
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(185)
 <223> n = A,T,C or G

<400> 26
 gnacnattgg caatgacnga aagaatttga angatgnaca agtnaaagnn acagtggcaa 60
 agaatcttcn gggcgcgta aaacaattgg gtgnatttaag gacaanctcg gtcancagta 120
 taanctctct ttcncgngga ttantngnca taatcatnat tctgacnngt aggacattnc 180
 caacc 185

<210> 27
 <211> 270
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(270)
 <223> n = A,T,C or G

<400> 27
 ttctggggct ctatacaggc tcttattnng atccangcgt gctgatgagt gcacagcacg 60
 atcacatctg gaaaccacca ntaccaccac cactacgcac ntcacaaaaa ctgtganagg 120
 gggcatttca gagacaanaa ttgaaaanccg aatagtcttc acgggggnat gcanacattg 180
 accatgacca ggcgctggct caggcagnta aagaggccan agatcaacac cctgacatgt 240
 cngtgaccag agtggtgggc cttacanaga 270

<210> 28
 <211> 758
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(758)
 <223> n = A,T,C or G

<400> 28
 tgctaggtan aaagttacct ctaaggggaag ctctgcagaa gaaatcagtg aaatactctg 60
 aaagccgcaa ttacaatcaa gaggaacctt ctccctcctt ggcaaagaaa cccaaggaag 120
 gcgagcgga gatttacttg gcaattgaaa gtgccaatga actggctgtg cagaaagcaa 180
 aggagaaat caccaggctc ataaaagaag agctgatccg gctgcaaaat tcataccaac 240
 caacaaataa aggaagatac aaagtcttat agacatccgg aaaaaagatt ttacctgtg 300
 ctggtctatg atgtatgtgg cagttgctgt ctgcagttta caatgtattg tnaatgaaga 360
 ttttttaaat tctatcttgc tgattttttt taaatataa aaactgggtac ttggtaaaga 420
 aatctgtccg taatttcccc ccaatcagtc caactatatt taaagccacc tglttttnaa 480
 ttttgatnrc clttaatgtt nactccaata tccatatttt aaatgtcccg gataatatcc 540
 caaagggtta aaaaatggaa atntttgaac ttcnnttgaa nanaataaat tcccatcctt 600

tangggntnt	ccccctnccc	gttcttccaa	gaaalgtagc	cttccccaaa	aaagntnate	660
cctanccttt	tgnttcccc	ctganlttct	gancccgagc	antnacgggt	ttaaaaanttt	720
ttaaattttc	caanncaaaa	aacctntnn	ttttttna			758

<210> 29

<211> 577

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(577)

<223> n = A,T,C or G

<400> 29

ctgctaggta	ntaanattat	ggatccacat	tgtnctgagg	anacgaanat	acttgctgct	60
gatngagggtg	aaaacgatat	tgatccntct	ggggttttac	ggigtgcact	gggtgctgca	120
cnnacttgtc	aagggtllgnt	acgtcctctg	ggcatctgca	aaaggccctg	ctctctggag	180
tgttgatgt	agtgtaccaa	aanagtattt	atacatccca	ccaatcaaaa	cacagctttt	240
ttacctcatg	cgaactcatn	caaaccaata	gaatntcaac	atgttctgta	ccttanagtg	300
ctcacttact	acctclgaac	natactcacg	ctgtnttttg	tctcttntct	atctttttgc	360
ntcttgtaat	taactctttg	tttcccttca	tcaaagttaa	tgtanatcgt	gatctattaa	420
aanaaaaatc	anggttgac	ttgctacttt	naanaaacccg	antgtggaaa	cattgggtct	480
naattcacac	aggatcngta	naactgttgt	ggatactgag	aaacntttga	atgttccctc	540
ccttattacc	atcccgcgaaa	aaaacccctn	tnntttt			577

<210> 30

<211> 449

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(449)

<223> n = A,T,C or G

<400> 30

tttaccat	aanntatagg	cgatagaatt	gatacctggc	gcaatagata	tagtaccgca	60
aggganagat	gaaaaattat	aacnaagcat	aatatagcaa	ggactaacc	ctatnccctn	120
tgcataatga	attaactaga	aataactttg	caaggagagc	caaagctaan	accnccgaaa	180
ccagacgagc	tacctangaa	cagctaaaag	agcacacccg	tctatglagc	anaatagtg	240
gaagattttat	aggttagaggc	gacaaacct	ccgagcctgg	tgatagctgg	tlgtccaaga	300
tagaatctta	gttcaacttt	aaatttgccc	acanaacct	ataaatcccc	ttgtaaattt	360
aactgttagt	ccaaagagga	acagctcttl	ggacactagg	aaaaaacctt	gtagagagag	420
tcataaaaaa	aanccctntn	gggnnnngn				449

<210> 31

<211> 500

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(500)

<223> n = A,T,C or G

```

<400> 31
tcttggaccc nggtcccccnn gngancaaaan aagaagggcn ngnttncaln gaaaancctg      60
tgattntcgc cccggtnacag gtgttnannit atggcccnch cncatctggg atacgcnaa      120
acaatntant tttaaatnnn gtnccccanc aaacaangtt cgtngnnttn actaggtagt      180
taatccncc ccatgttcaa ataaagggcc cgcgntncna ataaggaanc cnccccgant      240
ggggtcccg aggcctctc cttcataaaa nncattcaac ttccttcccn ctannaaagn      300
aattnttna atttttnaaa cactccctgt ccanggggac tttnccecca ntanctgaaa      360
aaatngcntg acgttcccc tccgctaag ggcnaactt anttncccc caanaccgcn      420
gggnnaggnn naaactcccc tngaaggga cnaactcgnt aaaaangga taatncccc      480
cnaattatc cctncccggg      500

```

<210> 32

<211> 426

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(426)

<223> n = A,T,C or G

```

<400> 32
gtctatgat acatctgacg ctattcttat ccccttctc cccgggacct ttccccctc      60
ctccctggga ccttttcccc ttctgttta anaanccagg gctgcctgga ggaagctttg      120
tcagatctag tggaatgtga cctccctgga atatgtgcc aggggtttgt ctaagcagtt      180
tcaggctatg gccttlactc catctggtec ccacccctct tatctctctc atgtgtggct      240
gcacctggac gcttggacca tagctgtcac agccccctgg ggaggaacct actccttggc      300
catnccagcc tgtgcaatgc aaggctcttg ttgatctgt gtgctgacan aaagcccagc      360
ttccttaaga acttttcatg tggaacactt tggttttgan aagaaaaala atcanaaacc      420
attaaa      426

```

<210> 33

<211> 375

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(375)

<223> n = A,T,C or G

```

<400> 33
ngttgcacct attggcngc tggctctgac tctgacctc gttatctgcc tgcctcggcc      60
tcctaaagtg ctgggattac aggagtgagc cacagtgcct ggctgtcaa gacttctctt      120
aagttaactt cclgagaagt galgtctaaa agtatctttg ctgggtgtgag aactccagtt      180
tccaacacat attatttccc tcaactatct ggaatatctt agaattttta ttccaaagga      240
ttagtctgaa tacaaglatg ccacataact cagttttcgc catcttncat ttcttaacag      300
tgtaaattaa aagctaataa tcataataat aaagtgcatt taattatctt cgaaaaaaaa      360
aaancccttt tgggg      375

```

<210> 34

<211> 809

<212> DNA

<213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(809)
 <223> n = A,T,C or G

<400> 34
 ttgcacatgc tggccaggat ggtctcgatc tcttgacctc gtgatctgcc cgcctcggcc 60
 tcccaaagtg ctggaactac aggtgtgagc caccacgcct ggcagctttg tgttcttttc 120
 lltctglgat cttgccttag atcacacaga taaaacatga caggacctgg accttaacac 180
 agttttggctc tcaatcctgt tctcataacc acnactgcct tcatttatct gtgtcatcct 240
 cagacctgac acatagtagg tgctcagtca gtgttcaacta agtaaatgat gaccaagaac 300
 tctttgactg ggtccaaggt gcttatccca ataactcgcc atggctacct ccttcattcc 360
 tcagctgact tgctctctct agcctggctg ctcctatttt atttcctaaa catggaccca 420
 tggcaataag tttaaancta acangttgat acggtaccca tccataattt aatnaattnt 480
 ggggctcatg caaccncaaa aaccagaacc caaaactacc tgtncncaaa caacaatcat 540
 tttnggtngg gatcccntnc tngcttggnc ccttttttta aaatgtccat tccccccgga 600
 cttaagaaa ttgaaggaat ncccggaan tattgttanc gggccccctt nagnaaaaaa 660
 ggtggcnctc cnncggggg cctccctgt cctgaaatt tnaaaacccc cctcccnntt 720
 taaanccctt aatcccggt aacancnaaa naaaattcta gggcccaaac ccanngggtt 780
 ggttttaaaa aacctntat ttttttnat 809

<210> 35
 <211> 192
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(192)
 <223> n = A,T,C or G

<400> 35
 caccttattg ggatacagca gtgaattaag ctattaaaat aagataatga ttgcttttat 60
 accttcagta gagaaaagtc lltgcatata aagtaatgtt taaaaaacat gtattgaaca 120
 cgacattgta tgaagcacia taaagattct gaagccaaaa aaaaaaaccc caanggggnt 180
 nnttttnaaa aa 192

<210> 36
 <211> 368
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(368)
 <223> n = A,T,C or G

<400> 36
 ctgctagtac caantattat ttaagantac ttttcaactac tcttaaataa tgacacagat 60
 acglltgccl tacacatttc actttattgt caagtlatta gtatgtttat ttccaaaagt 120
 tattttttgc aattttcttt tattattccg tactttttta atttacttca ttatcacgtc 180
 ttccctttat ctttttaaat agtttttgc tttgttatt ttgtttccct tttttactct 240
 tggtttgtaa tacccttttc ctatlltgc tttttctcat ttgatctcaa tgttaatcca 300
 actgttttcc acatctgat cactaaaatt ttaggccaaa aaaaaaanco cntttngggg 360

gngntttt

368

<210> 37

<211> 219

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(219)

<223> n = A,T,C or G

<400> 37

ggccccattt	cactctccat	antggcnctt	nctngaacag	gcgtncctga	tnagtgcaca	60
tacnalcaca	tcnaentgca	cctatanenc	ttccactacg	cacatcacca	aanctgtgaa	120
agggggcctn	tcnttagaca	cacaattgca	gaatngacnn	cncancccg	gggannctcn	180
angttcacen	tnagcaggn	gctggctcan	gctntttata			219

<210> 38

<211> 198

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(198)

<223> n = A,T,C or G

<400> 38

tcgatacagg	gncagatctg	ggagccaggg	cgttgctgat	gagttgcaca	gacgatcaca	60
tctgaaacca	ccagtaccac	caccactacg	cacatcacca	aagcgtggg	tcnggcaatt	120
aangaggcca	aagagcanca	cctgacatg	tongtgacnn	ttgtantggt	ccttaangac	180
acngacatcg	cctccaca					198

<210> 39

<211> 560

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(560)

<223> n = A,T,C or G

<400> 39

tttnnatcng	nacagctagt	cctntaaant	aatgactrca	tagaaatggc	attataattt	60
ttaagttgat	actctacagg	tagctatllg	lataaattagt	tttaataaaa	catgctgcaa	120
ccatggtata	caacaaaaat	acatttcctt	ggtgattgaa	allaaggcgg	tatttacaat	180
gacttaatat	aagactgact	tttatcctgc	ttcataactt	gtatggagaa	ctcaccaaga	240
aagaattcaa	tactgtgaaa	tatgcagcaa	gaagattggt	ctllacctag	gctgtgtttc	300
ctaagctctg	agtttttcagc	accagtagat	ttgtatttaa	agaaaaaaaa	atggggcctt	360
agcttctggc	ttttaatttt	gccagctaag	gacataaaaac	aaaantaanc	aancaaaaanc	420
aaatagccat	ntgctatcag	catcattatg	taaaagaaaa	tnatattttag	ccctaaaaat	480
taggaagaat	gtaatctcag	aataaagggt	glcattttaag	ttgaataaat	atntagcttt	540
cgaaaaaaaa	aanccctttt					560

<210> 40
 <211> 421
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(421)
 <223> n = A,T,C or G

<400> 40
 atacagggca gcggtgtagg tgaccacacc aggagcctca gcctcggtcc ttctcagccg 60
 tcgggataag atccagggcat gnccttttaaa tctcagaggt agcagtaaac ttttcantnt 120
 tgcngttagc aagtgtgtgt ttgccaatla ancccccaila tactaatgtg cctanttaat 180
 gttcagggaa natctgcttc cactgtgtnc cnaggggtgn catgaactnt gtgagnagcc 240
 ccnncnctgg agggatgaat gctgngttaa ctacngctat cacggatngt gtgntgtgaa 300
 naatacatcn acatnaatnl tannlgctct gnaanttccc ttnttatntg tcaagtaact 360
 ntttgtaaaa ntntnctcc caanttatta cngtgattac taatnnattn gtnccatggt 420
 t 421

<210> 41
 <211> 411
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(411)
 <223> n = A,T,C or G

<400> 41
 aggtagaggt tgtgcattgt gtccttttlla tctgatctgt gattaaagca gtaatatattt 60
 aagatggact gggaaaaaca tcaactcctg aagtttagaaa taagaatggg ttgtaaaatc 120
 cacagctata tctgatgct ggatggatt aatcttgtgt agtcttcaac tggtttagtgt 180
 gaaatagttc tgccacctcl gacgcaccac tgccaatgct gtacgtactg catttgcccc 240
 ttgagccagg lggatgttta ccgtgtgtta tataacttcc tggctccttc actgaacatg 300
 cctantccaa cattttttcc cagtggagtc ncacccctggg atccagtgtg taaatcccaa 360
 ttatcatgtc ttgtgcataa attcttccca aaagggatct ntaatttttt g 411

<210> 42
 <211> 408
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(408)
 <223> n = A,T,C or G

<400> 42
 ggctcccttc cctaactctc taagtacttc ccttaccac tcagtgtggg gatggcacct 60
 cctgaacttc cctgacaaat gogaacagga actccctatc atcaggagcc aacttgataa 120
 ctganaagat tctctctca ttatcagcc ttggattatc ttttgtgtc tcttactatt 180
 tgcgcttagc gagaaaaata aagaggtttg aacaattaag aagtaacaaa gagctcatag 240

```

ttcacaaaga gcaantcaaa ggatgtctgg aatatttgaa catacaactg cctttggcat 300
gaggtggcct acatacattc tcagggggcag gataggctgg nanagctgat caagctgccg 360
ggaaagctga agcaaaggca gggttggntg gaaatcaaaa tntctctt 408

```

<210> 43

<211> 275

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(275)

<223> n = A,T,C or G

<400> 43

```

tccctaactc tctaagtact tcccttacct actcagtgtg glgatggcac ctccctgaat 60
ctcctgacaa atgcgaacag gaactcctat tcatcagagc caacttgata actgagaaga 120
tccctctctc atttatcagc ctttgattat ctttttgtgt ctcttactat ttgcgcttag 180
caagaaaaat aaagaggttt gaacaantaa gaagtancnn ggagctenta gttcanaagn 240
agcaagtcaa aggatgtctg gangatttga aggggt 275

```

<210> 44

<211> 246

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(246)

<223> n = A,T,C or G

<400> 44

```

tttggctcca agcacatttc acaaangaga atttacacct agcacagctg glgocangan 60
atntcctang gacatggcca cctgggtcca ctccagcgac agacccctga caagagcagg 120
tctctggagg ctnantngca tggggcctan tntcttcaat cnaatgagcc ctnantgcta 180
ctgcgccccg ggggctccca cggcctgggc nntcttctntg caactgnaaa aggatagnng 240
tatttc 246

```

<210> 45

<211> 345

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(345)

<223> n = A,T,C or G

<400> 45

```

tttggctccg tgggacgttg tantgtgcnc agacatttcc aagggaaatt ctaaacaglc 60
acctnccct tttgcattcc cccaaatctt aagtgtatac ataaaacctt gggtacatat 120
tgltgtggtt atagaaggga attgggnaaa cngtacactt gttatatgga antractgtg 180
gccacctaca aaagacaagt taacaaaactg tontggaggc tgtngntgcc canccagggc 240
cgctgcnttt tgacaacatt cccacctgg ccactcagca canttcatgg caggtcatgt 300
ctntncaactg anacttttnt ganacttttl catatagcan aatcc 345

```

<210> 46
 <211> 969
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(969)
 <223> n = A,T,C or G

<400> 46
 aattgcagtt ctttcttgcc ttttaacaaca ttagggccctt tagaatgagt acctgggtgct 60
 gtcccttccaa ctctgtgatt ctctgattcc atccctcattt ttcaccalca ctgggtgtact 120
 ggcaagaacc antatgagat ttgaggaaaa atacttggat tactcttttt taaaaaaaat 180
 tatttagata taattcccat accatacaat taaccttttt atgtgtataa ttcagtattt 240
 ntagtatatc cacaaagtgt tgctaccatc accactatcc gattccagag cttgtcatca 300
 tacaaaaaaa aaaccccan agtnantlcc tttaaaaaan ctttnggttn ttcttntnc 360
 centgtngcn tctagnncng ngggnntnct tttgtcnntn tcnccctnch ctcattentn 420
 cnggtctctg ctengngnnn cgnntntgnt lnnanteget gctnntentg tatteccccgc 480
 nctngtnnng tctgcnnctg agccagtggg cctcctgntn ccnnengntt ctntntncgg 540
 cacanntcca nccanctgcc atnagtnana nnatctctnt tcnncanctg nttnncagnnt 600
 tgtctctctc tccgtncenc cngcngctnn ctenttncgc nctggngngc antcgtacct 660
 ggcttttatc cccclntcn nctnttctng atggntctc nctctnacac ctgncgttac 720
 gnntctctn tnnennnann cgttctctn tnncttncg nengccatct nagctcannc 780
 tggngcgant cncgctctgn gtatcagtca tntanagann ngngnnlgtt nccnncgcgn 840
 nntgagannc cccccnctt cgcctnacgt anglgncctt nttnnatctgc tegtctctc 900
 nctcatatcc nccatgctgn catganaact cntantctnn cgnnttctn negttccctc 960
 tgccctttn 969

<210> 47
 <211> 361
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(361)
 <223> n = A,T,C or G

<400> 47
 ggccactaag caggtcttac cnaatttaag aanattgaan tccctatcaag tatctcttct 60
 gaccacaatg gtatgaaact agaaatcagt aacaggagga aaattggaag altcacaaat 120
 ntgtggaant taatcaacnc atgagcaact antgagtcha agancanac aaaagggann 180
 tcaaaaactc tcttgagggtg gatgagaatg ganatacaac ataccngaac tcatgggatg 240
 tatcacaagc ngtgctaagg gggaagtta agtnctagat gtctanatta ngaaagggaa 300
 agatctcana tanacnacc agcnttncnc ctctgaanaac tagaaaaact aagaaaaaac 360
 t 361

<210> 48
 <211> 364
 <212> DNA
 <213> Homo sapien

<220>

<221> misc_feature
 <222> (1)...(364)
 <223> n = A,T,C or G

<400> 48
 atgatgacca catntagatg gcacatngat gaggacitla atctttcctt aaanacaata 60
 atgigtctctt ttttctttta ntcacatgat ttctaagtan attttncatg caggacactt 120
 tttcaacctt gatgtacant gactgtgtta aatttntctt tcagtggcaa cctctataat 180
 ctttannata tgggtgagcat ctngtctglt tagaanggga tatgacaata aatctatcag 240
 atggaaaatc ctgttacaaa gtataaaagc tttagtaatt tactcagtgt ggtgggttta 300
 tcctttttgc tttttctccc ltggtctata atgaaattgt tacagcagtg caaaataaaa 360
 tcct 364

<210> 49
 <211> 703
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(703)
 <223> n = A,T,C or G

<400> 49
 atggggaatc aaacaatggt aaaaggctan taatacttat aggttttatg attcaattta 60
 ctatgtgttt aaaattgltt ttgaaaaaa ttgagttatg tcnctaaaac tgagtctnta 120
 cagctcaaaa atgaagaaat acntatctcc gataagcata ttatgtgaat ttcaacatcn 180
 ctattgagaa aaggaatata aatttgaatg aaaatgaaac tctatctllc talatcacat 240
 tgcataagtg taggctagtg agtactttga tgtaaattgc tgtatctttt gaggentcna 300
 tttggcnata tagatcagaa ttttaaactn gcatactttg ttgcccagaa atctatcagg 360
 accacttgta ntatatttgt tnaaaggaa atcnaacnct tggatgttca nncagttatt 420
 gattgtttta naagaaggaa anggagaaag ggaggagaat ggaaganana aangggaggga 480
 ggaanattgg aacctttgac atntgtgata gcatnggatt tgctnaacac nctatantat 540
 acccctngca tggganaagc atgcacnctn aaacaaggac nngttngatg gntctacnnt 600
 ttgacntcag atnnaantaa atnaaaaaaa aaanccccc nctctttgnt ttctntcn 660
 cgnnnnnann ntctcccnc nncgncnnc ncccgcacc ntn 703

<210> 50
 <211> 413
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(413)
 <223> n = A,T,C or G

<400> 50
 tcttggcttg ttgagtattc aanaatcagg cagggagaag tggggtggat gcaaaccaac 60
 tgaccactgt ggcaccacca gcagtttcag ttttcatctt gantgtcnag aggaaatata 120
 taatcttaca actcnttagg ggctggctc agtggctcat acctgtntt cccancactt 180
 tgggagccg angcnggent atcaccgca ngtcaggatt ttgagaccac cctggccaac 240
 ntgggtgaaac cccatctcta ctantcaata caaancttag ctangcgtga tggcatgcac 300
 ctctaattcc acttactlgg gangctgagg cagcganaat cacttgtaac ccggaaggca 360
 nacgttgcat ntgagccaag atcgtgccac tgcactccat cctgggcltt cta 413

<210> 51
 <211> 252
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(252)
 <223> n = A,T,C or G

<400> 51
 gttacagaca aggnttntag aatatcttat gttttatgct ctgtaagttc aaagaagnta 60
 gcagaaaaca taagcatact gaaaagagaa acagaagcta ttttttaaat acctatgtga 120
 aatctctcta tntgaaacaa aaaatacact ggatggatta gacactgcag aaggaaaatt 180
 tggatgaactt gagatcttat aaataaaaat tatccaaaat gaagtgtaga gtgaaaaaaa 240
 aaaanccctt at 252

<210> 52
 <211> 875
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(875)
 <223> n = A,T,C or G

<400> 52
 agaaacgaga atgganattc aaatacgtcn gccgggcttg gtggattaga cctgtaaccc 60
 naacactttg ggaggnctag gtgggcggat caccngaggt cnnaggtacg ggaacancct 120
 ggcaaaaacc ccntctttan tctgngaaaa cncaactcta ctaaaanaac tactcttaga 180
 tnggcgtngn tgcgcctgcc tgtntccca gatacnnttl naggcctgang tggggataaa 240
 tnttttaaca tgggaagtgg aagtlgcact gatccaatgt ctccacactg cantccagcc 300
 tgggttangg aatgagaccc cncncacgga aaggacaata aaaancccn nnggnnttnn 360
 tttttaangg cctcttgntc ntnttctnt antgncgcc tncgcnncn ttgntntgtc 420
 gantcnntg cnntntttc tcnncctcn anctgcttc tntcnnttc gccntnnac 480
 ngcttcccc ntntctagc actnnnttc tntcgtccn nnatctccn ctntctnnn 540
 ccgctcgcgt nnnccntnan ctgntntc ncccttctt cncngcnncn ntctcgnca 600
 gatcgtncgn ctctatctac tctntccn gntntanata tngalnttac alntgtctcn 660
 atnaccatn annntctta tgtttatann ngtlnnnccn ttcaacnnnn cnttatgagn 720
 tcttnactca gctctncgtt gntntccna ctanngttg ncntncatgt nctgtncgt 780
 ancctctnc tcntcnngt cntgagacna atctctatnt alngnttatn cctgcntnct 840
 ganctncacc gngatctcgg cnnntcttc tcaag 875

<210> 53
 <211> 182
 <212> DNA
 <213> Homo sapien

<400> 53
 ccagaagaag ggctacatat ggactcatgt tgggcctact cctgcaataa caattaagga 60
 atcagttgcc aaccatttgt agltcacaaa tlaaaactgg gtttccagge ctggtgtggt 120
 ggctcacgcc tctagcccca gctattgcac cactgctctc caagctgggc aatggagtca 180
 ga 182

<210> 54
<211> 329
<212> DNA
<213> Homo sapien

<400> 54
catgatgcga gactggacat ctctcctacc ccatgtacac ttcagctgag caggcagaat 60
tagagagtca ggactagaag ttcagtctag ggatcaaata ataatagtag ctaatgttta 120
aagggtacct aagatccgcca ggagacatac tcagtatagt tccgtgggtt gccacatttc 180
atcttatcca gtagcacagg tgaaatttgt cttatgtgta tactgaggaa aaacaagtcc 240
ctctgatacc agcagccaat aaatgacaaa gctgggatag aaacttactt cattctaacc 300
cgagagtccc tgttcttgca tggggcaca . 329

<210> 55
<211> 312
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(312)
<223> n = A,T,C or G

<400> 55
actcaactcg tttgagctat aggaatnggc cattcgnngt ggctcanacc tgtaatccca 60
gnatttnggg anacctcact aggatcacnt gaggtcagga gttcaagacc agcctgtcca 120
acatgnggaa accccatctc tantanaaaa tacagaaatt atccaggtgt ggtggctggc 180
acctgtaatc ccagctactt gggaggccaa ggcattggaa attgtctgaa cctgggaagt 240
ggaggttgcg gtnanctgan atcatgccat tgcctctccag cctcggccac anataagac 300
cctatctcaa aa 312

<210> 56
<211> 565
<212> DNA
<213> Homo sapien

<400> 56
acaatttcac acaggaaaca gctatgacat gattacgaat ttaatacgac tcactatagg 60
gaattttggc ctcgaggcca agaattcggc acgaggggat ccaacgtcgc tccagctgct 120
cttgacgact ccacagatac cccgaagcca tggcaagcaa gggcttgag gacctgaagc 180
aacaggtgga ggggaccgcc caggaagccg tctcagcggc cggagcggca gctcagcaag 240
tggtggacca ggccacagag gcggggcaga aagccatgga ccagctggcc aagaccaccc 300
aggaaaccat cgacaagact gctaaccagg cctctgacac cttctctggg attgggaaaa 360
aattcggcct cctgaaatga cagcagggag acttgggtcg gctcctgaa atgacagcag 420
ggagacttgg gtgaccccc ttccaggcgc catttagcac agcctggccc tgatctccgg 480
gcagccacca cctcctcggg ctgccccctc attaaaaatc acgttcccaa aaaaaaaaaa 540
aaaaaaaaag atgcggccgc aagct 565

<210> 57
<211> 798
<212> DNA
<213> Homo sapien

<400> 57

ggaacaagta	gaagggaaga	gggaaatgga	gagcatcctt	atgactttac	aaaggggtgga	60
aatgaggatg	gagggataca	gaagtctgca	cagctgtaaa	ggttttatag	atgtctttgc	120
cttcccttct	gaggaaggga	agaagtaatg	aaagcacatg	tgaataaccc	cttccatccc	180
attcacagca	tgcactccc	agtccttaag	gcaaagggag	gcagtgtgta	agcattgggtg	240
gtgcagtgtg	aagagacaag	acctgatcat	ctgatcacac	ttgtgccaac	ttgattcata	300
ttgggcattt	ctaacaaccc	ctggtcaagg	taaataaggtt	gaacaatcaa	taacattatc	360
cctgcctgca	tacatgtgaa	caaaaqctat	agaggacatg	caaattctac	agtcattcct	420
catatgcttt	agacagagtg	cagclactgg	aatcttccag	atttcagtgt	ttlaaaatca	480
gagctctgaa	tacacaaaag	gaaagagaaa	tggagcagct	gacatafitt	aagctcacag	540
tgatactcag	tgacaggagc	acagagctct	aatgtccaca	ggatgttgta	gggtagggtc	600
tctcagtaaa	tcaagtccct	tacctatgtt	ctgacactga	ggctcttggg	gctatgggtt	660
agaaatccag	gaggcaatat	gctttlatte	taatgaagtc	ctcatcttgc	actcagaggc	720
ccactagttt	gcccttctat	atattaagta	aaaccaagag	aaattaaaaa	aaaaaaagcc	780
ctatagttag	tcttatta					798

<210> 58

<211> 729

<212> DNA

<213> Homo sapien

<400> 58

aagaatagac	cgagataggg	ttgagtgttg	ttccagtttg	gaacaagagt	ccactattaa	60
agaacgtgga	ctccaacgtc	aaagggcgaa	aaaccgtcta	tcagggcgat	ggcccactac	120
gtgaaccatc	accctaatac	agtttttttg	ggtcgagggtg	ccgtaaaagca	ctaaatcgga	180
accctaaggg	gagcccccga	tttagagctt	gacggggaaa	gccggcgaaac	gtggcgagaa	240
aggaagggaa	gaaagcgaaa	ggagcgggcg	ctagggcgct	ggcaagtgtg	gcggtcacgc	300
tgcgcgtaac	caccacaccc	gccgcgctta	atgcgcgct	acagggcgcg	tccattcgcc	360
attcaggctg	cgcaactgtt	gggaaggggcg	atcggtgcgg	gcctcttcgc	tattacgcca	420
gctggcgaaa	gggggatgtg	ctgcaaggcg	attaagttgg	gtaacgccag	ggttttccca	480
gtcacgacgt	tgtaaaaacga	cggccagtga	attgtaatat	gactcactat	agggcggaatt	540
gggcccctct	gatgcatgct	cgagcggcg	ccagtgatga	ggatatctgc	agaattcggc	600
ttglaatacg	actcactata	gggctttttt	ttttttcggt	ttgaggggga	atgctggaga	660
ttgtaatggg	tatggagaca	tatcataata	glaatgctag	tcttatectg	tgtgaaattg	720
ttatccgct						729

<210> 59

<211> 730

<212> DNA

<213> Homo sapien

<400> 59

aagaatagac	cgagataggg	ttgagtgttg	ttccagtttg	gaacaagagt	ccactattaa	60
agaacgtgga	ctccaacgtc	aaagggcgaa	aaaccgtcta	tcagggcgat	ggcccactac	120
gtgaaccatc	accctaatac	agtttttttg	ggtcgagggtg	ccgtaaaagca	ctaaatcgga	180
accctaaggg	gagcccccga	tttagagctt	gacggggaaa	gccggcgaaac	gtggcgagaa	240
aggaagggaa	gaaagcgaaa	ggagcgggcg	ctagggcgct	ggcaagtgtg	gcggtcacgc	300
tgcgcgtaac	caccacaccc	gccgcgctta	atgcgcgct	acagggcgcg	tccattcgcc	360
attcaggctg	cgcaactgtt	gggaaggggcg	atcggtgcgg	gcctcttcgc	tattacgcca	420
gctggcgaaa	gggggatgtg	ctgcaaggcg	attaagttgg	gtaacgccag	ggttttccca	480
gtcacgacgt	tgtaaaaacga	cggccagtga	attgtaatat	gactcactat	agggcggaatt	540
gggcccctct	gatgcatgct	cgagcggcg	ccagtgatga	ggatatctgc	agaattcggc	600
ttglaatacg	actcactata	gggctttttt	ttttttcggt	ttgaggggga	atgctggaga	660
ttgtaatggg	tatggagaca	tatcataata	glaatgctag	tcttatectg	tgtgaaattg	720
ttatccgcta						730

<210> 60
 <211> 623
 <212> DNA
 <213> Homo sapien

<400> 60
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 ttattgtctg catgatttta ggggatattg ggagggaaca agtagaaggg aagagggaaa 120
 tggagagcat ccttatgact ttacaaaggg tggaaatgag gatggaggga tacagaagtc 180
 tgcacagctg taaagggttt atagatgtct ttgccttccc tcttgaggaa gggaagaagt 240
 aatgaaagca catgtgaata accccttcca tcccatccac agcatcgcac tccagtcct 300
 taaggcaaag ggaggcagtg ctgaagcatt ggtggtgcag tglaaagaga caagacctga 360
 tcatctgatc acacttggtg caacttgatt catattgggc attactaaca acccctgggc 420
 aaggtaaata ggttgaacaa tcaataacat tatccctgcc tgcatacatg tgaacaaaag 480
 ctatagagga catgcaaatt ctacagtcac tcctcalatg ctllagacag agtgcagcta 540
 ctggaatctt ccagatttca gtgctttaa aacagagctc tgaatacaca aaaaaaaaaa 600
 gccctatagt gagtcgtatt aca 623

<210> 61
 <211> 376
 <212> DNA
 <213> Homo sapien

<400> 61
 gcatgctcga ggggcgcga gtgtgatgga tatctgcaga attcggctta ggggataaca 60
 attlccacac ggatccatga ctacagctatt aaggtctctg ccttggatcc ctatgaggaa 120
 tattttacca caggttcagc agaaggtaac ataaagggtt ggagattgac aggccattggc 180
 ctaattcatt catttaaaag tgaacatgct aagcagtcac tatttcgaaa cattggggct 240
 ggagtcatgc agattgacat catccagggc aatcggctct tctcctgtgg tgcagatggc 300
 acgctgaaaa ccagggttt gcccaatgct tttaacatcc ctaacagaat tcttgacatt 360
 ctataaagat tgggggt 376

<210> 62
 <211> 539
 <212> DNA
 <213> Homo sapien

<400> 62
 atgactcatt gtllctctgc ctttccgtgt gttacagggt ggctgatccc cctgcagcca 60
 gtttcccata agcaactgac ttccaaactg gaatgtctcg ggggataatg ggggtgggga 120
 tatggaagta tagagaaaac ataagaaaat actgggtgta tacacctttc tctctctgag 180
 tatgatgaca atgtgatagt cagtglggca tctgcgactc cagcttctgc ctggcatgta 240
 caccctagct ccagcttccc ctgggagact gtgcattctc tggctccact aacaccacct 300
 tcttctgacc ttccagccta gagatgatga ctctgccagc ctagalgggc tctgggttgt 360
 ctccctatcc ctggttgcct tgtagatttc ccattatgct gtcaccaact cccagccta 420
 agccctctct attttaaatt ctcaagtggg ttatgttccct gallagtcct lgactgatat 480
 accactctcc tcatgatctc tgattagttt tctgtttagg ttgttgcagt aaaaaaaaaa 539

<210> 63
 <211> 304
 <212> DNA
 <213> Homo sapien

<400> 63
 ggcttagcgg ataacaattt cacacaggac gactccaagc tgggaaggaa aattcccttt 60

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tccaacctgt atcaatTTTT acaactTTTT tctgaaagc agtttagtcc atactttgca      120
ctgacatact ttttccttct gtgctaaggt aaggatatcca ccttcgatgc aatccacctt      180
gtgttttctt aggggtggaat gtgatgttca gcagcaaaact tgcaacagac tggccttctg      240
tttgttactt tcaaaaggcc cacatgatac aattagagaa ttcccaccgc acaaaaaaaaaa      300
aaag                                          304

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<210> 64

<211> 226

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(226)

<223> n = A,T,C or G

<400> 64

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atgatgatga ccatgtggac agccaggact ccattgactc gaacgactct gatgatgtng      60
atgacactga tgattctcac cagtctgatg agtctcacca ttctgatgaa tctgatgaac      120
tggtcactga ttttcccneg gacctgceng caaccgaagt nttaactcca gttgtcccc      180
cagtagacac ntntgatggc cgaggtgatg gtgtggttta tggact                      226

```

<210> 65

<211> 225

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(225)

<223> n = A,T,C or G

<400> 65

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taccaacaga gcttctgaaa cagataccat agcattggag agaaaaacag ctcacagtct      60
gaggaagatg atattganag aaggaaagaa ttgaaagcat cttgaagaaa aactcagatt      120
ggaatntggga ttggtcaagt cggccggata atattcccc caaggagtcc ctctttaaac      180
accggaagcg cagggccacc ctacagcatga ggaacacgag cgtca                      225

```

<210> 66

<211> 240

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(240)

<223> n = A,T,C or G

<400> 66

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ccagcatggg ggccgtnatg gatagcgacc cacangcaag ctgggcttgg aggaattcaa      60
gtacttgagg aacaacatca aaagggtggca ggccatatac aaacagtacg acactgaccg      120
atcagggacc atgtgcagta gtgaactccc angtgctttt gaggcagcan ggttccacct      180
gaatgaacan ctctalaaca tgatcatccg acnctactca gatgaaagtg ggaacatgga      240

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<210> 67

<211> 504
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(504)
 <223> n = A,T,C or G

<400> 67
 cacgaggaga gatngcatct gctatatatt ccacngatac atgtgagtna ctgatagaaa 60
 aaatcgcnnc ggngaacact gncaccggtg ccggcccccg gtactacagg gatctcntca 120
 gacttcaccg tntactacaa ngtaagcncc ctttaagaat gtcacggagt atgatgggca 180
 ggatgectgc ggctccaaca nctggaacnt ggtggacgtg gacctcccgc ccaaraagga 240
 cntggagccc ggcatcttac tacatgggct gaanccctgg actcagtaag ccgtttacnt 300
 caaggctgtg accctcacca tgggtggagaa cgaccatata cgtggggcca agagtggagt 360
 cttgtncatt cgcnccantg cttcngttcc ttccttccc ttggaacnttc tttcggcacc 420
 aaactcctct tctcagttaa tctgaagtg gaacctccc tctctgccc acggcnacct 480
 gagttactac tttgtgcnct ggca 504

<210> 68
 <211> 462
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(462)
 <223> n = A,T,C or G

<400> 68
 tggatggcag ggggagaaa gaaaagcaaa acactccagg acctctccc gatctgtctc 60
 ctcctctagc cagcagtatg gacagctgga cccctgaact tctctcctc ttacctgggc 120
 agagtgttgt ctctcccaa atttataaaa actaaaatgc atnccattcc tctgaaagca 180
 aaacaaattc ataattgagt gatattaaat anagaggttt tcggaagcag atctgtgaat 240
 atgaaataca tgtgcatatt tcattcccca ggcagacatt tttlagaaat caatacatgc 300
 cccaatattg gaaagacttg ttcttccacg gtgactacag tacatgctga agcgtgccgt 360
 ttcagccctc atttaattca atttgtaagt agcgcagcag cctctgtggg ggaggatagg 420
 ctgaaaaaaa aaaanccct ttttngtnt nttttaaaaa aa 462

<210> 69
 <211> 357
 <212> DNA
 <213> Homo sapien

<400> 69
 agaagtcttc ctgagccttc catgtatcct cgggtgcccg ggattaacca gcgttatcaa 60
 ccaaagctaa aggatgatga ggttgctcag ctcaagaaaa gtggagatac cctgtgggac 120
 atccagaagg acctaaaaga cctgtgacta gtgagctcta ggctgtagaa atttaaaaac 180
 tacaatglat taactcgatc ctttagtttt catccatgta catggatcac agtttgcttt 240
 gatcttcttc aattgtgaat ttgggctcac agaataaaag cctatgcttg gtttaatgct 300
 tgcaatctga gctctgaac aaataaaatt aactattgta gtgtgaaaa aaaaaaa 357

<210> 70
 <211> 226

<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(226)
<223> n = A,T,C or G

<400> 70
atgatgatga ccatgtggac agccaggact ccattgactc gaacgactct gatgatgtng 60
atgacactga tgattctcac cagtctgatg agtctcacca ttctgatgaa tctgatgaac 120
tggtcactga ttttcccnng gacctgccng caaccgaagt ntctactcca gttgtccccc 180
cagtagacac ntntgatggc cgaggtgatg gtgtgggtta tggact 226

<210> 71
<211> 477
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(477)
<223> n = A,T,C or G

<400> 71
agcagacaag ccacaaltaa catagggtag aattgggtca tgtagctcat gggaaatcca 60
cagtcgtcaa agctatttct ggagttcata ctgtcaggtt caaaaatgaa ctagaaagaa 120
atattacaat caagcttgga tatgctaaty ctaagattta taagcttgat gacccaagtt 180
gccctcggcc agaattgtat agatcttggt ggagcagtag acctgacgag tttcctacgg 240
acattccagg gaccaaaggg aatttcagat tagtcagaca tgtttccttt gttgactgtc 300
ctggccacna tattttgatg gctactatgc tgaacgggtgc agcagtgatg gatgcagctc 360
ttctgttgat agctggtaat gaatcttgcc ctacgcctca gacatcgga acacctggct 420
gctatagaag atcatgaaac tgggaagccat attttgaatt ctacaaaata aaattga 477

<210> 72
<211> 374
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(374)
<223> n = A,T,C or G

<400> 72
ccaagccaga ttgtcactcc agctgatctt ctttgatggg gaagaggctt ttcttcaclg 60
gtctcctcaa gattctctct atgggtctcg acacttaact gcaaagatgg catcgacccc 120
gcacccacct ggagcgagag gcaccagcca actgcatggc atggatttat tggctctatt 180
ggatttgatt ggagctccaa acccaacggt tcccaatttt ttccanact cagccaggtg 240
gttcgaanga cttcaagcan ttgaacatga acttcatgaa ttgggtttgc tcaangatca 300
ctctttggag gggcggtatt ccanaatta cagttatgga ggtgtgattc aggatgacn 360
ttttccattt ccaa 374

<210> 73
<211> 597

<212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(597)
 <223> n = A,T,C or G

<400> 73
 ccaagggatc tgtaaagaat atataacttga gtgggtgtgtg ttatcagata aagcacccctg 60
 tatcacagac tggcaacaag aagatgggtac cgtgcatcgc acctatttaa gagggaaactt 120
 agcagagagc aaatgctatt lgataacagt tactccagta tatgctgatg gaccaggaag 180
 cccctgaatcc ataaaggcat accttaaaca agctccacct tccaaaggac ctactgttcg 240
 gacaaaaaaaa gtaggggaaaa acgaagctgt cttanagtgg gaccaacttc ctgttgatgt 300
 tcanaatgga tttatcagaa attatactat attttatana accatcattg gaaatgaaac 360
 tgctgtgaat gtggattctt cccacacaga aatntacatt gtctcttttg actagtgaca 420
 cattgtacat ggtacgaatg gcagcataca cagatgaagg tgggaaggat ggtccaaaat 480
 tcacttttac tacccecaan tttgctcaag gganaaattg aagccatant cgtgcctgtt 540
 tgcttancat tctattgac aactcttctg ggaatgctgt tctgctttaa taagcga 597

<210> 74
 <211> 257
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(257)
 <223> n = A,T,C or G

<400> 74
 tggtaaaagg taatagccag agnntagaac cttgangaga tgcggccaan gattctttat 60
 atctgaaccn agatgtnaaa naagaaaatg ctttgaggct ttctaagcga tctctctgtc 120
 taattttncac ctttgtcttg atgcacactt ctgacncgc tgccacaacc tgtggggctc 180
 gatgtgtccc ttgatgggtg cggccctcag ggactgcacc ctgacaagtg tttaggcaan 240
 attcctttct tgtgcc 257

<210> 75
 <211> 330
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(330)
 <223> n = A,T,C or G

<400> 75
 tggtcataag gctgggtgata naggggtctt gtcattggaaa ggtgctcttc caggaaacct 60
 ctgtgtatgg aggtcgnagc cacaatacgc ggacgangat glgaacacct acaatgccgc 120
 catccttac accatcctca gccaaagatcc tgagctccct gacnaaaata tggtcncat 180
 taacagggaac gcaggagtca teggtgtggt cncactggg ctggaccgaa agagtttccc 240
 tacgtgtacc ntgggtggtc aagcngctga ccttcanggt gaggggttaa tcacnacagc 300
 ancngctgtg atcacagtea ctgntaccaa 330

<210> 76
 <211> 387
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(387)
 <223> n = A,T,C or G

<400> 76
 gctcgcgcgc ctgcaggctc acactagtgg atccaaagaa ttccggcagc gaacaacagt 60
 tatctccaag atgctattcg ttgaacccat cctggagggt tccagcttgc cgacaaccaa 120
 ctcaacaacc aattcagcca ccaaaataac agctaatacc actgatgaac ccaccacaca 180
 acccaccaca gagcccacca cccaacccac catccaaccc acccaaccaa ctaccagct 240
 cccaacagat tctcctaccc agcccactac tgggtccttc tgcccaggac ctgttactct 300
 ctgctctgac ttgganantc attcaacana agccgtgttg ggggaagctt tggtaaattt 360
 ctccctgaag ctctaccacg ccttctc 387

<210> 77
 <211> 339
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(339)
 <223> n = A,T,C or G

<400> 77
 ctgctgaten gggtcctttt ggagcacaga tgatgcnatg gccanennng gacaacnacg 60
 tgatctgcgc cctggctctg gtgtccatnc tggccctcgg nancctggcc gagggccana 120
 canagacgtg tncagtggcc ccccgtaaaa gacagaattg tggttttcct ggtgtcacac 180
 cctcccantg tgcaataaag ggctgctgtt tgcacaacac cgttcgtggg gtccctcgtt 240
 gcttctatcc taataccntc nactlccnc canaaaagga ntgtgaattt tanacacttc 300
 tgcagggatc tgcttgcac ctgacgcngt gccgtcccc 339

<210> 78
 <211> 385
 <212> DNA
 <213> Homo sapien

<400> 78
 tcggtcatag ggagagattt gtatgctgta ctatgcagcg tttaaagtta gtgggttttg 60
 tgatttttgc attgaatatt gctgtctgtt acaaagtcag ttaaaggtag gttttaatat 120
 ttaagtatt ctatcttga gataaaatct gtatgtgcaa ttcaccggtt ttaccagttt 180
 attatgtaaa caagagattt ggcattgacat gttctgtatg tttcaggga aaatgtcttt 240
 aatgcttttt caagaactaa cacagttatt cctatactgg attttaggtc tctgaagaac 300
 tgctggtgtt taggaataag aatgtgcatg aagcctaaaa taccaagaaa gcttatactg 360
 aatttaagca aaaaaaaaaa acccc 385

<210> 79
 <211> 307
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(307)
 <223> n = A,T,C or G

<400> 79
 tcgatacagg gatgtcagag ctgccagaga ctttatcctg aagctttacc aagatcagaa 60
 tcctgacaaa gnagaaagtc atctactctc acttcacatg tgctacagat acagacaata 120
 ttcgctttgt gtttgctgct gtcaaagaca caattctaca gctaanccta aggggaattca 180
 accttgctta aaagctgctg cccactcctc ccctataaca gaagatgtga tttgcaaact 240
 ccttggttta ttignaagtg cttctgacat cncagagcc agcccatgc caggaactaa 300
 ggatgtc 307

<210> 80
 <211> 528
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(528)
 <223> n = A,T,C or G

<400> 80
 gtcgatacag gaacagcatg tccaaatcga tgtggatgtt tccaagcctg acctcacggc 60
 tgccctgcgt gacgtacgtc agcaatatga aagtgtggct gccagaacc tgcaggaggc 120
 agaagaatgg tacaaatcca agtttgctga cctctctgag gctgccacc ggaacaatga 180
 cgccctgcgc caggcaaagc aggagtccac tgagtaccgg agacagggtg agtccctcac 240
 ctgtgaagtg gatgccctta aaggaaccaa tgagtccctg gaacgccaga tgcgttgaaa 300
 tgggaagagaa ctttgccggtt gaagctgcta actaccaaga caclattggc cgctgcagg 360
 atgagattca gaatatgaag ganggaaatg gctcgtcacc ttcgtgaata ccaagacctg 420
 ctcaatgtta agatggccct tgacattgaa attgccacct acanggaact gctggangcn 480
 aagaaaacca ggatttctct gcctcctcct aacttttctt cccctgaa 528

<210> 81
 <211> 369
 <212> DNA
 <213> Homo sapien

<400> 81
 agcatggctc ccgaagtttt gccaaaacct cggatgcgtg gccttctggc caggcgtctg 60
 cgaaatcata tggctgtagc attcgtgcta tccctggggg ttgcagcttt gtataagttt 120
 cgtgtggctg atcaaagaaa gaaggcatac gcagatttct acagaaacta cgatgtcatg 180
 aaagattttg aggagatgag gaaggctggg atctttcaga gtgtaaagta atcttggaa 240
 ataaagaatl tcttcagggtt gaattaccta gaagtttgtc actgacttgt gttcctgaac 300
 tatgacacat gaatatgtgg gctaagaaat agttcctctt gataaataaa caattaacaa 360
 aaaaaaaaa 369

<210> 82
 <211> 269
 <212> DNA
 <213> Homo sapien

<220>

<221> misc_feature
 <222> (1)...(269)
 <223> n = A,T,C or G

<400> 82
 atgacagggga tgancaaaact lnglclggggg tattgatgaa gatgacctac tgctgatgat 60
 accagtgcgtg ctgtaactga agaaatgccca ccccttgaaag gagatgacga cacatcacgc 120
 atggaagaag tagactaatac tctggctgag ggatgactta cctgttcagt actclacaat 180
 tcctctgata atatatatttc aaggatgttt ttctttattt ttgttaatat taaaangtct 240
 gtntggnatg acaactnctt taaggggaa 269

<210> 83
 <211> 196
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(196)
 <223> n = A,T,C or G

<400> 83
 tttgggtcca attacagcta aagcaaaagt ggttattgaa ctgtttttat cggctctcggg 60
 nnttgctaaa ccttcccagg tgtattttgg aggtacagtt gttggcnagc aagctatnaa 120
 atctgaagat gaagtgggaa gtnaatana gtatgaatnc agggtaagaa actnaggtaa 180
 acctnaata tncctc 196

<210> 84
 <211> 448
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(448)
 <223> n = A,T,C or G

<400> 84
 caaacatggg catgggtgtca gcgataatgt ttntancagc tcccagacata aatcagtaan 60
 tnngatttcc accatatcha ncntcnggaa ttttaaccntc aggagnagct cttnttcaga 120
 cnccttgga aaacgagccc cattgnancc anctttgana cataaaacct ggagaaattc 180
 tccaatacng aaggtatana gcggggcctc gttgacagca tcacgggtca aaggcttctg 240
 gaggtcagg cctgcaaagg tggcatcatc caccacaacca cgggccagaa cctgtcnctt 300
 caggacgcag tctcccnngg tgtgattgac caagacatgg ccaccaggct gaagcctgct 360
 cagaaagcct tcataggctt cgagggtgtg aaggggaaaga agaagatgtc agcagcagag 420
 gcagtgaanaa aaaaaaaacc cctatatt 448

<210> 85
 <211> 169
 <212> DNA
 <213> Homo sapien

<400> 85
 agcagaccaa ctgccttttg tgagaccttc cctccctat ccccaacttc aaaggtgtga 60
 gagtattagg aaacatgagc agcatatggc ttttgatcag ttttccagtg gcagcatcca 120

atgaacaaga tcctacaagc tgtgcaggca aaacctagca ggaaaaaaaa

169